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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

February 4, 2006, 12:09:23 ; Search time 199 Seconds (without alignments) 397.428 Million cell updates/sec Run on:

US-09-529-206E-4 959 Title: Perfect score:

1 MOAEGRGTGGSTGDADGPGG........NITQCFLPVFLAQPPSGQRR 180

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

2443163 seqs, 439378781 residues Searched:

2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003bs:* geneseqp2004s:* geneseqp2005s:* geneseqp2002s:* geneseqp2003as:* A Geneseq 21:* 1: geneseqp1980s:* 2: geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES		Description	4 Aaw62584 Cancer a	Aaw69665	Aay05965	Aay52430 Human	Aay70862 Human	Aab03154	6 Aab69946	Aag67164 Amino	Aau01535 Human	Aae07714	.8 Aau84818 Human NYN	3 Aaul1543 Human tum	2 Abr58672 Human can	Abr48210 Human	Abu56508 Lung o	Abu56694	Abp74198		6 Adc09576 NY-ESO-1	8 Add35568 Human NY	Add25510		Adj54139	
SUMM		Ð	AAW62584	AAW69665	AAY05965	AAY52430	AAY70862	AAB03154	AAB6994	AAG67164	AAU01535	AAE07714	AAU84818	AAU11543	ABR58672	ABR48210	ABU56508	ABU56694	ABP74198	ABR83438	ADC09576	ADD35568	ADD25510	ADN39068	ADJ54139	
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		Score	959	959	959	959	959	959	959	959	959	959	959	959	959	959	959	959	959	959	959	959	959	959	959	
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Adq18451 Human sof Adq10446 Autoimmun	Ads80926 Tumour as Adw44353 Human aut	•	Aea35651 Human NY-	Aae13122 NY-ESO-IC	_	Aeb80047 Human NY-	Abu64816 Human NY-	Adz28913 NY-ESO-1	Adz42374 Immunogen	Adm73418 CAG-3 pro	Adm73417 Human NY-	Adk68648 Epitope l	Add35564 Human NY-	Abp74199 Human LAG	Adc09577 LAGE-1a p	Adm72816 Human LAG	Aaw69664 Human LAG	Aay70860 Human LAG
ADQ18451 ADQ10446	ADS80926 ADW44353	ADY85096	AEA35651	AAB13122	ADW99402	AEB80047	ABU64816	ADZ28913	ADZ42374	ADM73418	ADM73417	ADK68648	ADD35564	ABP74199	ADC09577	ADM72816	AAW69664	AAY70860
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									36									

ALIGNMENTS

Cancer associated antigen; NY-ESO-1; regression; progression; onset; cancer; treatment; diagnosis. /note= "potential myristorylation site" 'note= "potential myristorylation site" note= "potential phosphorylation site" 'note= "potential phosphorylation site" Location/Qualifiers Cancer associated antigen NY-ESO-1. AAW62584 standard; protein; 180 AA. (first entry) Key Misc-difference Misc-difference Misc-difference Misc-difference Homo sapiens. 17-SEP-1998 AAW62584; AAW62584

'note= "potential phosphorylation site" /note= "potential phosphorylation site" Misc-difference Misc-difference

WO9814464-A1 09-APR-1998.

97WO-US016335. 15-SEP-1997; 96US-00725182. 03-OCT-1996; (LUDW-) LUDWIG INST CANCER RES

Jager E, Knuth A; Chen Y, Scanlan M, Gure A, Old LJ, Drijfhout JW;

WPI; 1998-286417/25.

N-PSDB; AAV38566.

New isolated cancer associated antigen - is used to develop products for the diagnosis and treatment of cancers and for monitoring cancer therapy.

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The present sequence represents a cancer associated antigen. The clone from which the DNA sequence is obtained is designated NV-ESO-1. The specification described a method for determining regression, progression of onset of a cancerous condition, comprising monitoring a sample from a patient with the cancerous condition for a parameter selected from NY-ESO-1 protein, a peptide derived from NY-ESO-1 protein and cytolytic T cells specific for the peptide and an MHC molecule with which it non-covalently complexes. Methods for the treatment of a cancerous condition are also described. The NY-ESO-1 protein and peptides derived from it can be used for diagnosis and treatment of cancers and to monitor the efficacy of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLLKEFTVSGNILTIRLTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQPPSGQRR 180
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                                                                                                                                                                                                                                                                                                                                                                                                Length 180;
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                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 959; DB 2; 100.0%; Pred. No. 5.9e-79;
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                        Claim 8; Fig 3; 49pp; English.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                         therapeutic regime
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Gaps

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New isolated LAGE-1 tumour associated nucleic acids - used to develop products for the diagnosis and treatment of LAGE-1 associated disorders, particularly tumours.
                                                                                                                                                        Boon-Falleur T;
                                                                                                                                                       Lethe B, Lucas S, De Smet C, Godelaine D,
                                                                                                                                          (LUDW-) LUDWIG INST CANCER RES
                                                                                                                             97US-00791495.
                                                                                                                                                                     WPI; 1998-427951/36.
                                                                                                                                                                           N-PSDB; AAV50348.
                                                                                                                             27-JAN-1997;
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Claim 4; Fig 3A; 88pp; English.

The present sequence represents human NY-ESO-1, formerly known as LL-1.2 clone, which is used in an example from the present invention which describes LAGE-1 tumour associated protein (TAP). The present invention also describes: (1) a method for treating a subject with a disorder

Example 2; Page 57-58; 73pp; English.

characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering to the subject autologous cytolytic T cells to ameliorate the disorder, where the cytolytic T cells are specific for complexes of an HLA molecule and a LAGE-1 TAP or an immunogenic fragment; (2) a method for treating a subject with a disorder characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering a LAGE-1 TAP or an immunogenic fragment to ameliorate the disorder; and (3) a method for selectively enriching a population of T cells with cytolytic T cells specific for a LAGE-1 TAP comprising contacting an isolated population of T cells with an agent presenting a complex of a LAGE TAP or an immunogenic fragment and a HLA presenting molecule to selectively enrich immunogenic fragment and a HLA presenting molecule to selectively enrich immunogenic fragment and a HLA presenting molecule to selectively enrich contact and a HLA presenting molecule to selectively enrich methods and products from the present invention can be used for the methods and treatment of LAGE-1 associated disorders, particularly ö 61 PRGPHGGAASGINGCCRCGARGPESRLLBFYLAMPFATPMEABLARRSLAQDAPPLPVPG 120 121 VLLKEFTVSGNILTIRLTAADHROLOLSISSCLOOLSLLMWITQCFLPVFLAQPPSGORR 180 PRGPHGGAASGINGCCRCGARGPESRILERFYLAMPFATPMEAELARRSLAQDAPPLPVPG 120 9 NY ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; parcreatic cancer; liver cancer; tumour; diagnosis; immunotherapy; therapy; vaccine; ORFI. 1 MOAEGRGTGGSTGDADGPGGPGIPDGPGGNAGGPGEAGATGGRGPRGAGAARASGPGGGA 1 MOABGRGTGGSTGDADGPGGPGIPDGPGGNAGGPGEAGATGGRGPRGAGAARASGPGGGA Gaps ö Length 180; Indels ; Human cancer antigen NY ESO-1/CAG-3 ORF1 protein. Query Match
Best Local Similarity 100.0%; Pred. No. 5.9e-79;
Matches 180; Conservative 0; Mismatches 0; (USSH) US DEPT HEALTH & HUMAN SERVICES. AAY05965 standard; protein; 180 AA Cancer antigen NY ESO1/CAG-3. 97US-0061428P 16-AUG-1999 (first entry) SA; WPI; 1999-277270/23. Wang RF, Rosenberg N-PSDB; AAX58599 Sequence 180 AA; WO9918206-A2. 21-SEP-1998; 08-OCT-1997; Homo sapiens 15-APR-1999, 61 AAY05965; tumours RESULT 3 AAY05965 8888888888888888888888 ò 셤 ઠે 셤 ò

Pept 1de

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The present sequence represents the ORF1 protein encoded by open reading frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides comprising ORF1, ORF2 (see AAY05966), portions of these peptides and their variants (see AAY05965-AAY05966), portions of these peptides and their variants (see AAY05965-CAAY05966), portions of these peptides and their variants (see AAY05965-CAAY05966), portions of these peptides and their variants (see AAY05965-CAAY05966), portions of these peptides that inhibit expression of the cancer peptide, useful in diagnostic and detection assays; and methods of cancer peptide, useful in diagnostic and detection assays; and methods of the cancer peptide or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, or lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, liver cancer, and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Malanoma is treated by inducing cancer-specific T cells in vitro for subsequent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMRAKLARRSLAQDAPPLPVPG 120
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Pred. No. 5.9e-79;
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and HLA-B35"
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Unidentified
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15-FEB-2000
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"Peptide presented by MHC Class I HLA-A24 and HLA-
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                                                                   'note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
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:e= "Peptide presented by MHC Class I HLA-B44"
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te= "Peptide presented by MHC Class I HLA-B44"
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/note= "Peptide presented by MHC Class I HLA-B52"
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                            "Peptide presented by MHC Class I HLA-A1"
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98US-00165546.
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                                                                                and HLA-B35"
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Ritter G;
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Klade C;

Heider K,

Aarnoudse CA,

Schrier PI,

WPI: 2000-339685/29

N-PSDB; AAD00152

(UYHO-) UNIV HOSPITAL LEIDEN.

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This sequence represents a human turmour antigen, NY-ESO-1, the cDNA encoding which was isolated from an oesophagus squamous cell cancer CDNA library. Tissue localisation studies revealed it to be expressed at high levels in normal ovary and testis but not in normal colon, kidney, liver, brain, oesophagus and skin. It was expressed in certain turmours and turmour cell lines, and breast and bladder cancer specimens, with expression in other turmour types being sporadic. Peptides derived from NY ESO-1 are bound by both MHC (major histocompatibility complex) Class I and culles for presentation to T-cells. Peptides AAY52431- 52434 bind to Class I HIA-A2 molecules, thereby stimulating peptides AAY52431- 52543 bind to Class I HIA-A2 molecules, while peptides AAY52435-Y52440 bind to Class II HIA-DR53 molecules, stimulating helper T-cell proliferation. The peptides derived from NY-ESO-1 may be used in methods and compositions used for the treatment, diagnosis and prevention of cancers (such as melanoma, breast cancer, bladder cancer, lung cancer, hepatoma, contain cancer, bladder cancer, or lymphoma) and to
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                                                  Novel peptides which bind to MHC class I and MHC class II molecules, useful for therapeutic and diagnostic purposes.
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Best Local Similarity 100.0%; Pred. No. 5.9e-79;
Matches 180; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human tumour antigen, NY-ESO-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stimulate the proliferation of T cells
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                                                                                                            Claim 30; Fig 3; 49pp; English.
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2000-038483/03
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Best Local Similarity
                 N-PSDB; AAZ38380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 180 AA;
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The present sequence is the human NY-ESO-1 protein, a tumour antigen, identified by screening an esophagus carcinoma cDNA library. This protein is derived from open reading frame (ORP)-1 that contain epitopes of tumour specific T-cells NY-ESO-1 is expressed in different tumour types, but not in healthy tissues except in testis. It also shows homology with the CAMEL (Cytotoxic T lymphocytes (CTL)-recognised Antigen on MELANOMA) protein, a tumour-asociated antigen. The tumour-associated antigen. The tumour-associated antigen. This sequence has anticancer activity. CAMEL tumour antigen and finamunogenic peptides derived from it are useful for cancer immunotherapy. They have the potential to induce an immune response, by eliciting a CTL response. The DNA molecule is used for the construction of recombinant or
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                                                                                                                       Tumor-associated antigen useful for cancer immunotherapy is encoded by the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 959; DB 3; Length 180;
100.0%; Pred. No. 5.9e-79;
ive 0; Mismatches 0; Indels
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/note= "Potential O-phosphorylation site"
138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Potential O-phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human oesophageal cancer-associated antigen NY-ESO-1.
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                                                                                                                                                                           Example 3; Page 62-63; 73pp; English.
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Best Local Similarity
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NY-ESO-1; CAMEL, CTL-recognised Antigen on MELanoma; human; cancer; CTL; cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer; melanoma; immunotherapy; immune response.

(BOEH) BOEHRINGER INGELHEIM INT GMBH.

99WO-EP007832 98EP-00119583

15-OCT-1999; 16-OCT-1998;

27-APR-2000

WO200023584-A1

Homo sapiens

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This sequence represents a human oesophageal cancer-associated antigen, NY-ESO-1. The CDNA encoding this sequence was isolated from a CDNA library prepared from a specimen of well-to-moderately differentiated squamous cell cancer of the oesophageal Expression analysis demonstrated that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma cell lines and in normal ovary and testis tissue, but not in normal colon, kidney, liver or brain tissue. Analysis of the amino acid sequence of the protein indicates that the protein has a transmembrane domain, several N-myristoylation sites and O-phosphorylation sites and that it contains antigen; sequences in the N-terminal half of the protein. The antigen is useful as an immunogen when combined with an adjuvant, in both precursor and post-translationally modified forms, and may be used to precursor and post-translationally modified forms, and may be used to generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic marker for oesophageal cancer, and can be utilised as a marker for the targetted delivery of therapeutic agents to oesophageal cancer cells. It can also be used to generate diagnostic or therapeutic agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated esophageal cancer-associated antigen useful as markers for producing antibodies and as targets for identifying abnormal conditions, e.g. infections and cancer.
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/note= "Potential O-phosphorylation site"
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                152. .172
/note= "Potential transmembrane domain"
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                                                                                                                                                                                                                                   (SLOK ) SLOAN KETTERING INST CANCER RES (CORR ) CORNELL RES FOUND INC. (LUDW-) LUDWIG INST CANCER RES.
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N-PSDB; AAA61483.
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                                                                                                                                                         26-JAN-1998;
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                                                                                                                 30-MAY-2000
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The present sequence is human NY-ESO-1 protein. It is provided in a specification relating to a method for determining the status of a cancerous condition in a patient with a tumour that expresses NY-ESO-1. The method comprises assaying a sample taken from the patient for antibodies that specifically bind to the NY-ESO-1 and comparing the value obtained to a prior value obtained from assay of a prior sample taken from the patient. Any difference between the values is indicative of a change in status of the cancerous condition. The method is useful for determining whether a cancerous condition is progressing, regressing or remaining stable, in particular in patients receiving treatment for a melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
                                                                                                                                                                                                                                                                                                                                                                                                                    regression or
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                                                                                                                                                                                                                                                                                                                                                                                                                 Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining the levels of NY-ESO-1 specific antibodies in a sample taken from a
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            Human, NY-ESO-1, HLA, human leukocyte antigen, CTL; cytotoxic T cell; HLA-A2, HLA-DR53, melanoma, adenocarcinoma; bladder carcinoma; non-small cell lung carcinoma; tumour status determination.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 959; DB 4;
100.0%; Pred. No. 5.9e-79;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                            Old LJ, Knuth A,
                                                                                                                                                                                                                                                        (LUDW-) LUDWIG INST CANCER RES.
(SLOK ) SLOAN KETTERING INST CANCER RES.
(CORR ) CORNELL RES FOUND INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Fig 3; 50pp; English.
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                                                                                                                                                                                       14-JUL-2000; 2000WO-US019220.
                                                                                                                                                                                                                         99US-00359503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
nes 180; Conservative
                                                                                                                                                                                                                                                                                                                              Stockert B,
                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-182822/18.
                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAF58634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 180 AA;
                                                                                                                    WO200107917-A1
                                                                                                                                                                                                                       23-JUL-1999;
                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-NOV-2001
                                                                                                                                                                                                                                                                                                                              Jager B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG67164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     patient
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'note= "Myristoylated"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II; major histocompatibility complex; helper T cell; HLA-DR; cancer; major maior antigen-determining region; disease progression; disease regression; disease onset; body tissue; body fluid; enzyme label; radioactive label; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRGPHGGAASGINGCCRCGARGPESRILEFYLAMPFATPMEAELARRSLAQDAPPLPVPG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAELARRSLAQDAPPLPVPG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLLKEPTVSGNILTIRLTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQPPSGQRR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VILKEFTVSGNILTIRLTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQPPSGQRR 180
                                                                                                                                                                                                                                                                                                      The present sequence represents cancer testis tumour antigen NY-ESO-1 datas called LAGE-2). NY-ESO-1 is a molecule that is processed to at least one human leukcoyte antigen (HLA) binding peptide, which binds to class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis, but not normal colon, Kidney, liver or brain tissue. The presence or level of expression of NY-ESO-1 may be assayed for the diagnosis of cancer, especially testis tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen; HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour; cancer; testis tumour.
                                                                                                                                                                                                                                           mmic sequences of tumor associated antigen {\tt EY-ESO-1} (LAGE-2) useful diagnosing testicular tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOAEGRGTGGSTGDADGPGGPGTPDCPGGNAGGPGEAGATGGRGPRGAGAARASGPGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MQAEGRGTGGSTGDADGPGGPGIPDGPGGNAGGPGEAGATGGRGPRGAGAARASGPGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 959; DB 4; Length 180; 100.0%; Pred. No. 5.9e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human NY-ESO-1 tumour rejection antigen precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU01535 standard; protein; 180
                                                                                                                                                                                                                                                                                 Example 5; Fig 3; 50pp; English.
                                                                                                                                                                (LUDW-) LUDWIG INST CANCER RES
                                                                                                                    22-JAN-2001; 2001WO-US002126.
                                                                                                                                          22-FEB-2000; 2000US-00510635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 180; Conservative
                                                                                                                                                                                       Lethe B, Boon-Falleur
                                                                                                                                                                                                             WPI; 2001-550091/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                         N-PSDB; AAH75118
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 180 AA;
                                                                        WO200162917-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                  Homo sapiens
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                                                                                             10-AUG-2001
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The sequence represents a human NW-ESO-1 tumour rejection antigen

CC precursor. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to

Drecursor. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to

CC major histocompatibility complex (MHC) Class II molecules such as human

CC class II HAD-NY-ESO-1/SSX-2 complex expressed on the surface of a cell

CC class II HIAD-NY-ESO-1/SSX-2 complex expressed on the surface of a cell

CC class II HIAD-NY-ESO-1/SSX-2 complex expressed on the surface of a cell

CC class II HIAD-NY-ESO-1/SSX-2 complex expressed on the surface of a cell

CC class II HIAD-NY-ESO-1/SSX-2 complex expressed on the surface of a cell

CC class II HIAD-NY-ESO-1/SSX-2 complex expressed on the surface of a cell

CC class II HIAD-NY-ESO-1/SSX-2 complex expressed on the surface of a cell

CC class II HIAD-NY-ESO-1/SSX-2 complex expressed on the surface of a cell

CC class II HIAD-NY-ESO-1/SSX-2 complex present in the tell munical complex present in the complex or tissue) can be monitored for the amount of the complex present in the complex of a cancerous condition. The method involves contacting the sample consective labelled or enzyme labelled monoclonal antibody which

CC specifically binds with the complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEABLARRSLAQDAPPLPVPG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptides binding to major histocompatibility complex class II human leukocyte antigen-determining region molecule having amino acid sequence found in tumor rejection antigen precursor used for stimulating proliferation of helper T cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VILKEFTVSGNILTIRLTAADHRQLQLSISSCLQQLSLLMWITQCFLFVFLAQPPSGQRR
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100.0%; Score 959; DB 4;
Best Local Similarity 100.0%; Pred. No. 5.9e-79;
Matches 180; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                /note= "Phosphorylated"
                                                                                                             "Phosphorylated"
                                                                                                                                                                                          'note= "Phosphorylated"
                                                                                                                                                                                                                                                                       /note= "Phosphorylated"
                                    'note= "Myristoylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tureci O, Sahin U, Pfreundschuh M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Fig 3; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-SEP-2000; 2000WO-US026411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-00408036.
                                                                                                                 'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-266156/27
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                                                                                                                                                                                                                                                                                                                                                                                                                             WO200123560-A2
Modified-site
                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                     Modified-site
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180

RESULT 10 AAE07714

Location/Qualifiers

Key Modified-site

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The invention relates to the identification and isolation of major histocompatibility (MHC) class II restricted T cell epitope (MHC-II epitopes opitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HAA-DR or HLA-DP crestricted. The products of the gene are promising candidates for immunotherapeutic strategies for the prevention, treatment and diagnosis of patients with cancer. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T lymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection from metastasis, or by inhibiting the growth of cells expressing the NY-ESO-1 gene product. The cancer peptides are also useful as diagnostic agent to detect the presence of cancer, to enhance the generation of antibody and/or CD8+ T cell responses against any given target antigen and/or hapten and to induce tumour-specific humoral-mediated immunity against cancer. The present sequence is human NY ESO-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eptide or MHC class II restricted T cell epitopes, and vaccine for inhibiting cancer in a mammal or as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MQAEGRGTGGSTGDADGPGGPGI PDGPGGNAGGPGEAGATGGRGPRGAGAARASGPGGGA
                                                                                                                                                     Human; major histocompatibility complex; MHC; vaccine; metastasis; class II restricted T cell epitope; MHC-II epitope; cancer antigen; NHY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; tumour-specific humoral-mediated immunity; cancer; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 180;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 959; DB 4;
100.0%; Pred. No. 5.9e-79;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                       /note= "Encoded by CCCGGGGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
AAE07714 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NY-ESO cancer peptide or MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 1; 134pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JAN-2000; 2000US-0179004P
29-SEP-2000; 2000US-0237107P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-496851/54.
N-PSDB; AAD14179, AAD14180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful as immunogen and vac
protection from metastasis.
                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 180; Conservative
                                                                                                                  Human NY BSO-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang R, Rosenberg SA,
                                                                                                                                                                                                                                                                                                                                 Misc-difference 45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                              WO200155393-A2
                                                                                                                                                                                                                                     immunotherapy
                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                             06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                     02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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New synthetic polypeptides having several different segments of at least one parent polypeptide linked together differently compared to the linkage in the parent polypeptide, for inducing immune response against a
121 VLLKEFTVSGNILTIRLTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQPPSGQRR 180
           Savine, vaccine, cancer, viral infection, HIV, hepatitis C virus, viral infection; human immunodeficieny virus, melanoma; bacterial infection, Salmonella, Legionella; parasitic infection,
                                                                 AAU84818 standard; protein; 180 AA
                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Fig 27; 364pp; English.
                                                                                                                         Human NYNSOla consensus sequence.
                                                                                                                                                                         Trypanosoma; Toxoplasma; Giardia.
                                                                                                                                                                                                                                                   25-MAY-2001; 2001WO-AU000622.
                                                                                                                                                                                                                                                                      26-MAY-2000; 2000AU-00007761.
                                                                                                                                                                                                                                                                                        (AUSU ) UNIV AUSTRALIAN NAT.
                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                            Ramshaw IA;
                                                                                                                                                                                                                                                                                                                              WPI; 2002-147575/19.
                                                                                                                                                                                                                                                                                                                                                                               pathogen or cancer.
                                                                                                                                                                                                             WO200190197-A1
                                                                                                                                                                                           Homo gapiens
                                                                                                     08-MAY-2002
                                                                                                                                                                                                                                 29-NOV-2001.
                                                                                                                                                                                                                                                                                                             Thomson SA,
                                                                                   AAU84818;
                                              RESULT 11
                                                       AAU84818
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The invention relates to a new synthetic polypeptide (I) comprising several different segments of at least one parent polypeptide linked cogether in a different relationship relative to that linkeds in the parent polypeptide to impede, abrogate or otherwise alter at least one parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide and for inducing an immune response against a pathogen or cancer. Also included are a synthetic polymucleotide encoding and a computer system for designing the synthetic polypeptides. The synthetic polypeptides and polymucleotides or synthetic polypeptides. The synthetic polypeptide is useful for are referred to as a Savine. The synthetic polypeptide is useful for cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head cancer, (e.g., ranain, testicle, uterus), as potentiating agents.

Compositions comprising the polypeptide may be used in the treatment or prophylaxis against viral (such as infections caused by HIV (human cuirus), hepatitis, influenza, Japanese encephalitis cuirus, Epstein-Barr virus and respiratory and yencytial virus), bacterial cuirus, Epstein-Barr virus and respiratory syncytial virus), bacterial cuirus, Epstein-Barr virus and respiratory syncytial virus), bacterial cuirus, infections caused by Neisseria, Meningococcal, Haemophilus, compositions caused by plasmodium, Schobacterium or parasitic control caused by plasmodium, Schobacterium or parasitic cuirus, the consensus sequence for a parent protein used to design a savine of the incontrol.

Sequence 180 AA;

8 9

Gaps

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1 MOAEGRGIGGSTGDADGPGGPGIPDGPGGNAGGPGEAGATGGRGPRGAGAARASGPGGGA

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Gaps ö Query Match 100.0%; Score 959; DB 5; Length 180; Best Local Similarity 100.0%; Pred. No. 5.9e-79; Matches 180; Conservative 0; Mismatches 0; Indels

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PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAELARRSLAQDAPPLPVPG 120
                                                                                                                                                                    61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPWEAELARRSLAQDAPPLPVPG 120
                                                                                                                                                                                                                                                          121 VILKEFTVSGNILTIRLTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQPPSGQRR 180
                                                                                                                                                                                                                                                                                               121 VLLKEFTVSGNILTIRLTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQPPSGQRR 180
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                                     MQAEGRGTGGSTGDADGPGGPGT PDGPGGNAGGPGEAGATGGRGPRGAGAAARASGPGGGA
MQAEGRGTGGSTGDADGPGGPG1 PDGPGGNAGGPGEAGATGGRGPRGAGAARASGPGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human tumour associated antigen NY-ESO.
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2000US-00561074.
2000US-00561571.
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28-APR-2000; 2000US-00561571.
28-APR-2000; 2000US-00561572.
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AAU11543
LIT AAU11.
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virus, HIV, infection, hepatitis virus and papilloma virus), cancers virus, HIV, infection, hepatitis virus and papilloma virus), cancers (e.g. tumours), lancerion, hepatitis virus and papilloma virus), cancers (e.g. tumours), lancerion of calls by intracellular parasites (e.g. tumours), infection of calls by intracellular parasites (e.g. the specification. The invention permits the vaccine designer to ignore peptides that, despite predicted high binding affinity for MHC, will never be useful because they cannot be presented by target cells. The invention provides a major advance in vaccine design, one that combines the power of antigen sequence analysis with the fundamental realities of immunology. The invention allows for the simple and effective selection of meaningful epitopes for creation of MHC class I or Class II vaccines using any polypeptide sequence corresponding to a desired target. The present sequence is an HLA-A2.1 (human leukocyte antigen) presenting target call protein from which epitopes of the invention may be derived, NY-ESO (a tumour associated antigen)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 959; DB 5;
100.0%; Pred. No. 5.9e-79;
cive 0; Mismatches 0;
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2001US-0323887P.
2001US-0350666P.
2002US-0355145P.
2002US-0355257P.
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N-PSDB; ACC72823.
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Best Local Similarity
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20-SEP-2001;
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08-FEB-2002;
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The invention relates to a vaccine comprising a first housekeeping epitope derived from a first antigen associated with a first target cell. Also included are an isolated T cell expressing a T cell receptor specific for a major histocompatibility complex (WHC) -peptide complex comprising a first housekeeping epitope which is derived from a first antigen associated with a first target cell, selecting an epitope (or peptide sequence) from a population of peptide fragments of an antigen associated with a target in a host, where the fragments have a known or predicted affinity for a MHC receptor peptide binding cleft of the host, where the epitope selected corresponds to a product of proteolytic cleavage of the antigen in a cell of the host and a nucleic acid construct comprising a first coding region, where the first coding region construct comprises a first sequence encoding at least a first polypeptide, where the first polypeptide comprises a first housekeeping epitope derived from a first antigen associated with a first target cell; The epitopes, peptides, vaccines and nucleic acids are useful in the manufacture of a

Example 23; Fig 17; 131pp; English.

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Human; bladder cancer; cytostatic; gene therapy; vaccine.
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                      Claim 12; Page 757-758; 767pp; English.
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                                                                                                                                                                                                                                                                                  ABR48210 standard; protein; 180
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03-AUG-2001; 2001US-0310099P.
08-NOV-2001; 2001US-0343705P.
13-NOV-2001; 2001US-0350666F.
12-APR-2002; 2002US-0372246P.
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                                                                                                                                                                           Best Local Similarity 100.
Matches 180; Conservative
                                                                                                                                                          Sequence 180 AA;
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The present invention describes a method for detecting a bladder cancerassociated transcript in a cell from a patient. The method comprises contacting a blological sample from the patient with a polymuclecide that selectively hybridises to a sequence that is 80 % identical to a cabe of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059 concode the human bladder cancer-associated proteins given in ABR48146 to ABR48142). Bladder cancer-associated proteins given in haR848146 to ABR48142). Bladder cancer-associated proteins given in haR848146 to have cytostatic activities, and can be used in antisense gene therapy and in vaccine production. The method can be used in antisense gene therapy and cancer-associated transcript in a cell from a patient. The method is useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in various screening and diagnostic methods, and for gene therapy, vaccine and/or antisense/inhibition applications
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                                                                                                                                                                         Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with bladder cancer-associated polynucleotide or antibody.
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100.0%; Pred. No. 5.9e-79;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                              Claim 10; Page 278; 307pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                 Aziz N;
                                                                                                                        N-PSDB; ACC51024
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                                 Mack DH,
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                                                                                                                                                            The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-regulated in a psecific cancers (e.g. about 1031 genes up-regulated in a related yellowing the proteins given in ABRSS910, Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising a nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically trargeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a patient by administering to the patient the antibody above; and (7) a patient by administering to the patient, the nucleic acid is useful for the appeautic targets. In particular, the nucleic acid is useful for diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, bladder, braain, breast, cervix, colon/rectum, kidney, lung, ovary, clangers, prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in chrost prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in chrost pathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAELARRSLAQDAPPLPVPG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PRGPHGGAASGINGCCRCGARGPESRILEFYLAMPFATPMEABLARRSLAQDAPPLPVPG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLLKEFTVSGNILTIRLTAADHRQLQLSISSCLQQLSLLAWITQCFLPVFLAQPPSGQRR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
genes that are up-regulated or down-regulated in cancers, useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MQAEGRGTGGSTGDADGPGGPGIPDGPGGNAGGPGEAGATGGRGPRGAGARASGPGGA
                           markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MOAEGRGTGGSTGDADGPGGPGIPDGPGGNAGGPGEAGATGGRGPRGAGAARASGPGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IndelB
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Gaps

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120

18-APR-2001; 2001US-0284770P. 18-APR-2002; 2002WO-US012476.

(EOSB-) EOS BIOTECHNOLOGY INC

31-OCT-2002.

09-NOV-2001; 2001US-0339245P. 13-NOV-2001; 2001US-0350666P. 29-NOV-2001; 2001US-0334370P. 12-APR-2002; 2002US-0372246P.

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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits to a sequence that is at least 80 % identical to a gene that exhibits confered polymucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell controlities, chronic obstructive pulmonary disease, fibrosis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, bronchiectasis. The genes, polymucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences
                                                                                                                                                                                                                                                                                 Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polymucleotide that exhibits increased or decreased expression in lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                    27; Page 270; 453pp; English.
                                                                                                                   (EOSB-) EOS BIOTECHNOLOGY INC.
                                                                                                                                                                                                              WPI; 2003-093161/08.
N-PSDB; ABX76232.
                                                                                                                                                                    Murray R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
                                                                                                                                                               Aziz N,
                                                                                                                                                                                                                                                                                                                                                                                                         Claim
%X66666666666666666666668
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Sequence 180 AA;

9 1 MQAEGRGTGGSTGDADGPGGPGTPDPGPGGNAGGPGEAGATGGRGPRGAGAARASGPGGGA 60 MQAEGRGTGGSTGDADGPGGPGI PDGPGGNAGGPGEAGATGGRGPRGAGAARASGPGGGA Gaps ö Length 180; 0; Indels 100.0%; Score 959; DB 6; 100.0%; Pred. No. 5.9e-79; iive 0; Mismatches 0; Query Match Best Local Similarity 100.8 Matches 180; Conservative 8 ď

PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATFMEAELARRSLAQDAPPLPVPG 120

à

Search completed: February 4, 2006, 12:13:10 Job time : 201 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

February 4, 2006, 12:13:27; Search time 42 Seconds (without alignments) 412.358 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-529-206E-4 959 1 MQAEGRGTGGSTGDADGPGG......WITQCFLPVFLAQPPSGQRR 180

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	polyketide hydroxy	la costa protein -		hypothetical glyci	alp	alph	ical	~	~	cal	~	hypothetical prote	hypothetical prote	glycine-rich prote	collagen alpha 1(I	collagen - chicken	hypothetical prote		hypothetical glyci				hypothetical glyci	tractin - medicina	glycine-rich prote	collagen alpha 1(X	hypothetical glyci	_	Н
	Ωī	T35608	T08435	QQBE31	B70807	CGB01S	CGHU1S	D70807	F70806	T32812	H70589	T32734	T27525	T20605	S01821	CGCH1S	150629	T21070	F85584	E70806	T24590	CGHU1E	KNIMU	A70896	T18531	S19932	B31795	A70934	G70917	E70917
	BB	~	~	Н	~	Н	-	7	~	~	~	N	7	~	ч	Н	ď	N	~	~	~	Н	Н	~	~	~	~	~	~	7
	Length	627	145	641	1079	779	1464	1489	1901	530	615	1215	297	299	252	1042	473	296	440	1381	290	1806	338	853	1880	228	482	1306	741	1329
* Query	_ :	18.2	16.2	16.2	16.0	15.9	15.8	15.7	15.7	15.7	15.6	15.6	•	15.5	15.5	15.5	15.4	15.3	15.3	15.3	15.3	15.3	15.2	15.2	15.2	15.2	15.2	15.2	15.1	15.1
	Score	174.5	155.5	155.5	153	152.5	151.5	151	151	150.5	149.5	149.5	149	149	148.5	148.5	147.5	147	147	147	146.5	146.5	146	146	146	145.5	145.5	145.5	145	145
Result	No.	7	7	m	4	Ŋ	9	7	80	σı	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote collagen 2 - Caeno	hypothetical prote	probable tail fibe	myosin heavy chain	hypothetical glyci	collagen alpha 1(I	hypothetical prote	hypothetical glyci	collagen alpha 1(I	collagen alpha 1(I	hypothetical prote	probable tail fibe	probable tail fibe	hypothetical glyci	glycine-rich prote
T24586 B31219	T26004	D90734	MWAXIB	A70893	150696	T32247	A70807	I50694	CGB07S	T19142	H90854	C90769	A70869	T49893
0 0	~	N	Н	~	N	N	~	~	н	N	N	N	N	N
301	330	438	1147	667	310	314	714	988	1049	323	437	439	1660	244
15.1		15.1	15.1	15.0	15.0	15.0	15.0	15.0	15.0	14.9	14.9	14.9	14.9	14.9
	15.1													142.5 14.9

ALIGNMENTS

-		
_	RESULT 1	
_	T35608	
	polyketide hydroxylase - Streptomyces coelicolor	
_	C;Species: Streptomyces coelicolor	
-	C;Date: 05-Nov-1999 #sequence revision 05-Nov-1999 #text_change 09-Jul-2004	
	C;Accession: T35608	
	R; Seeger, K.J.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.	A.
_	submitted to the EMBL Data Library, June 1999	
-	A; Reference number: Z21584	
_	A;Accession: T35608	
	A;Status: preliminary; translated from GB/EMBL/DDBJ	
	A; Molecule type: DNA	
-	A;Residues: 1-627 <see></see>	
	A; Cross-references: UNIPROT: P42534; UNIPARC: UPI000012CFEE; EMBL: AL079356; PIDN: CAB45603.3	603.1
_	A; Experimental source: strain A3(2)	
	C; Genetics:	
_	A;Gene: SCOEDB:SCGG9.12c	
_	C; Superfamily: tetracycline 6-hydroxylase	
	Query Match 18.2%; Score 174.5; DB 2; Length 627;	
	Best Local Similarity 42.7%; Pred. No. 4.1e-06; Matches 47; Conservative 4; Mismatches 28; Indels 31; Gaps 6;	
	Qy 5 GRGTGGSTGDADGPGGPGIPDGPGGNAGGPGEAGATGG-RGPRGAGAARASGPGGAPRG 63	
	OY 64 PHGGAASGLNGCCRCGARGPESRILEFYLAMPFATPMEAE 103	
	Db 463 PGGGPORILINVALGYRYPRGAVVGADPATPVVPE 498	

RESULT 2

la costa protein - fruit fly (Drosophila melanogaster)
C.Species: Drosophila melanogaster
C.Accession: T08435
R.Maleszka, R.; de Couet, H.G.; Miklos, G.L.
Proc. Natl. Acad. Sci. U.S.A. 95, 3731-3736, 1998
A.Fritle: Data transferability from model organisms to human beings: insights from the fur A.Reference number: Z16415; MUID:99188272; PMID:9520435
A.Fritle: Data transferability from GB/EMBL/DDBJ
A.Fression: T08435
A.Fr

10;

Length 1079;

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A,Molecule type: DNA
A,Residues: 1-1079 <COL>
A,Cross-references: UNIPARC;UPI0000D3AEA; GB:AL022022; GB:AL123456; NID:g3261554; PIDN:C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                collagen alpha 1(I) chain - bovine (tentative sequence) (fragments)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius (cattle)
C;Accession: A91193; A91229; A91201; A91201; A91200; A43048; A02853
R;Rauterberg, J.; Timpl, R.; Furthmayr, H.

Bur. J. Blochen. 27, 231-237, 1972
A;Fitle: Structural characterization of N-terminal antigenic determinants in calf and hum A;Reference number: A91193; MUID:72255334; PMID:4115172
                                                                                                                                                                                                            A,Gene: Rv3512
C,Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    480 AGGTGGAGGTGGAAGDGGQGGQGGAGGAGGAGGAGGAGGAGGAGGNGGNITGGTAGTAGAAAG 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 AEGRGTGGSTGDADGPGGPGIPDGPGCNAGGPGEAGATGGRGPRG-----AGAARASG
                                                                                                                                                                                                                                                                                                                                                                                                                   39; Indels
                                                                                                                                                                                                                                                                                                                                 16.0%; Score 153; DB 2;
43.3%; Pred. No. 0.0003;
:ive 2; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 PGGGAPR---GPHGGAASGLNGCCRCGARG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 563-675 <WEN>
A;Cross-references: UNIPARC:UP10000173B55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 295-562 <FI3>
A;Cross-references: UNIPARC:UP10000173B54
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A;Residues: 146-294 <FI2>
A;Cross-references: UNIPARC:UP10000173B53
                                                                                                                             A; Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 43.34
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein A; Residues: 1-19 <RAU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nuclear antigen EBNA1 - human herpesvirus 4
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 25-Feb-1985 #sequence revision 25-Feb-1985 #text_change 09-Jul-2004
C;Accession: C43043; S42440; A3773; S33021
R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
Mol. Biol. Med. 1, 21-45, 1983
A;Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus
A;Reference number: A33065; MuID:85035713; PMID:6092825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: $42440
A;Status: preliminary
A;Nolecule type: mRNA
A;Nolecule type: mRNA
A;Residues: 1-66 <SAM>
A;Cross-references: UNIPARC:UPI0000170E9C; EMBL:M13941; NID:g330399; PIDN:AAA45889.1; PI
C;Superfamily: Epstein-Barr virus nuclear antigen
C;Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
By 1980
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A;Residues: 1-641 <BAN>
A;Cross-references: UNIPROT:P03211; UNIPARC:UPI00000CDDD; EMBL:V01555; NID:959074; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Experimental source: strain B95-8
R;Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.;
Nature 310, 207-211, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A; Reference number: A03794; MUID:84270667; PMID:6087149
A; Contents: annotation; protein coding region
F; Sample, J; Hummel, M; Braun, D; Birkenbach, M; Kieff, E.
Froc. Natl. Acad. Sci. U.S.A. 83, 5096-5100, 1986
A; Title: Nucleotide sequences of mRNAs encoding Epstein-Barr virus nuclear proteins: a
A; Reference number: S42440; MUID:86259739; PMID:3460083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
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                                                                                                                                                                             17 GPGGPGIPDGPGGNAGGPGEA----GATGGRGPRGAGAARASGPGG-GAPRGPHGGAASG
                                                                                           Gaps
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                                                                                      Indels 11;
Length 145;
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46.2%; Pred. No. 0.00012;
ive 1; Mismatches 41;
    Score 155.5; DB 2;
Pred. No. 3.1e-05;
0; Mismatches 24;
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    Query Match
Best Local Similarity 51.4%;
Matches 37; Conservative
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les 37; Conservative
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Matches
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A;Cross-references: UNIPROT:P02453; UNIPARC:UPI0000173B51
A;Experimental source: skin
A;Note: the epsilon carbon of Lys-9, by homology with the rat alpha 1(I) chain, is conven
B;Fietzek, P.F.; Kuehn, K.
Bicchem. 52, 77-82, 1975
A;Title: The covalent structure of collagen: amino-acid sequence of the cyanogen-bromide
A;Reference number: A91229; MUID:76022320; PMID:1164916
                                                                                                                                                                                                                                                                                                                          A;Accession: A91229
A;Molecule type: protein
A;Residues: 20-145 <FIE>
A;Residues: 20-145 <FIE>
A;Residues: 20-145 <FIE>
A;Residues: 20-145 <FIE>
A;Roserimental source: skin
A;Note: Lys-103 is hydroxylated and binds glucosylgalactose
A;Fietzek, D.P.; Wendt, P.; Kell, I.; Kuehn, K.
FEBS Lett. 26, 74-76, 1972
A;Fittle: The covalent structure of collagen: amino acid sequence of alphal-CB3 from calf
A;Reference number: A91387; MUID:73049499; PMID:4673951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Experimental Bource: skin
R;Fietzek, P.P.; Rexrodt, F.W.; Hopper, K.E.; Kuehn, K.
Bur, J. Blochem. 38, 396-400, 1973
A;Title: The covalent structure of collagen. 2. The amino-acid sequence of alphal-CB7 from A;Reference number: A91211; MUID:74086118; PMID:4359390
A;Accession: A91211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Experimental source: skin
R;Wendt, P.; Mark, K.V.D.; Rexrodt, F.; Kuehn, K.
Brix. J. Biochem. 30, 169-183, 1972
A;Title: The covalent structure of collagen. The amino-acid sequence of the 112 residues
A;Reference number: A91201; MUID:73042276; PMID:4343808
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m

Page

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A, Molecule type: protein
A, Molecule type: protein
A, Residues: 759-779 < RA2>
A, Erosidues: 759-779 < RA2>
A, Erosidues: 759-779 < RA2>
A, Experimental source: skin
C, Comment: Dysines at positions 115, 124, 274, 346, 424, 496, 658, and 670 may be hydrox
C, Comment: Prolines in the third position of the tripeptide repeating unit (G-X-Y) are H
C, Comment: The order of the eight CNBr peptides in the alpha 1(1) chain of bovine skin of 9, 149, 268, and 217 residues.
C, Comment: The complete chain contains 1052 residues.
C, Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology; C, Keywords: coiled coil; extracellular matrix; glycoprotein; pyroglutamic acid; trimer; F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-472 <TRO>
A; Cross-rences: UNIPARC:UPI000016A6F9; EMBL:X07884; NID:g30015; PIDN:CAA30731.1; PID
A; Note: submitted to the EMBL/GenBank/DDBJ databases by Prockop, D.J., 13-UUN-1988
R; Chu, M.L.; de Wet, W.; Bernard, M.; Ding, J.F.; Morabito, M.; Myers, J.; Williams, C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collagen alpha 1(1) chain precursor - human
N;Alternate names: procollagen alpha 1(1) chain
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 160114; S01143; A93335; I55254; A39943; I55237; A35233; S09400; B90567; S11
5269; A29439; I53466; A02852; I37247
S269; A29439; I53466; A02852; I37247
S269; A29439; I53466; A02852; I37247
S269; A29439; I53466; A02852; I37247
S47; A16-115, 1988
A;Title: Complete nucleotide sequence of the region encompassing the first twenty-five e A;Title: Complete nucleotide sequence of the region encompassing the first twenty-five A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Status: Lranslated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Cross-references: UNIPROT:P02452; UNIPROT:Q14992; UNIPROT:Q16053; UNIPROT:Q13896; UNIPROT:Q18896; UNIPROT:Q1896; UNIPR
Figure 1. Biochem. 30, 163-168, 1972

Bur. J. Biochem. 30, 163-168, 1972

A;Title: The covalent structure of collagen. Amino acid sequence of peptide alphal-CB6-CA; 1971

A;Reference number: A91200; MUID:73042275; PMID:4343807

A;Accession: A91200

A;Accession: A91200

A;Accession: A91200

A;Residuas: 676-758

A;Cross-references: UNIPARC:UP10000173B56

A;Cross-references:UNIPARC:UP10000173B56

A;Cross-references:UNIPARC:UP1000173B56

A;Cross-references:UNIPARC:UP10000173B56

A;Cross-references:UNI
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A,Molecule type: DNA
A,Residues: 1-58, Q', 60-181 < CHU>
A,Residues: 1-58, Q', 60-181 < CHU>
A,Cross-references: UNIPARC: UP10000173B3C; EMBL: X00820; NID: g35657; PIDN: CAA25394.1; PID: R,Rossouw, C.M.S.; Vergeer, W.P.; du Plocy, S.J.; Bernard, M.P.; Ramirez, F.; de Wet, W.i. J. Biol. Chem. 262, 15151-15157, 1987
A,Title: DNA sequences in the first intron of the human pro-alpha 1(I) collagen gene enh?
A,Reference number: I55254; MUID: 88033098; PMID: 2822714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-45 < ROS>
A; Cross-references: UNIPARC: UPI000016A6B2; GB:J02829; NID:g180387; PIDN:AAA51993.1; PID:g180387; PIDN:AAA51993.1; PID:g180340: 1-45 < ROS>
A; Cross-references: UNIPARC: UPI000016A6B2; GB:J02829; NID:g180387; PIDN:AAA51993.1; PID:g18037389; PID:g1803789; PID:g1803789; PID:g1803789; PID:g180376; PIDN:AAA52052.1; PID:g1803789; PID:g180376; PIDN:AAA52052.1; PID:g1803789; PID:g180376; PIDN:AAA52052.1; PID:g1803789; PID:g1803789; PID:g180376; PIDN:AAA52052.1; PID:g1803789; PID:g1803789; PID:g180376; PIDN:AAA52052.1; PID:g1803789; PI
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A; Robedidues: 1.34 (-CH12>
A; Robedidues: 1.34 (-CH12>
A; Cross-references: UNIPARC: UPI000016A6B1; GB:M10627; NID:g180383; PIDN: AAA51992.1; PID:c
R; Wirtz, M.K.; Keene, D.R.; Hori, H.; Glanville, R.W.; Steinmann, B.; Rao, V.H.; Holliste
J. Biol. Chem. 265, 6312-6317, 1990
A; Title: In vivo and in vitro noncovalent association of excised alphal(I) amino-terminal rome, type VII.
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A, Molecule type: mRNA
A, Residues: 156-130 * MBL3
A, Cross-references: UNIPARC: UP10000173B3E
A, Cross-references: UNIPARC: UP10000173B3E
B, Click, E.M.; Bornstein, P.
B, Choss-references: UNIPARC: UP10000173B3E
B, Click, E.M.; Bornstein, P.
B, Choss-references: UNIPARC: UP10000173B3E
A, Title: Isolation and characterization of the cyanogen bromide peptides from the alpha1
A, Reference number: A00567; MUID: 11038625; PMID: 5229814
A, Contents: CNBr0-1, CNBr2, CNBr4, CNBr5
A, Cross-references: UNIPARC: UP10000173B3F
A, Residues: 162-198, 'Z', 200-201, 'Z', 203-206, 'Z', 208-209, 'Z', 211-228, 'B', 230, 'BB', 233, 'Z', A), Cross-references: UNIPARC: UP10000173B3F
A, Experimental source: skin
A, Note: evidence for 170-allysine
A, Note: evidence for 170-allysine
B, Notebohm, H.; Bodo, M.; Deutzmann, R.; Mueller, P.
Bur. J. Biochem: 192, 153-159, 1990
A, Title: A critical crosslink region in human-bone-derived collagen type I. Specific cles
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A;Residues: 175-187;274-287,'P',289 <BAE>
A;Cross-references: UNIPARC:UP10000173B40; UNIPARC:UP10000173B41
A;Note: sequence of collagen alpha 1(S)(I) isolated from bone after pepsin digestion
R;Deak, S.B.; Scholz, P.M.; Amenta, P.S.; Constantinou, C.D.; Levi-Minzi, S.A.; Gonzalez-J. Biol. Chem. 266, 21827-21832, 1991
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A, Cross-references: UNIPARC: UP10000173B3D
A, Note: this propeptide fragment remained non-covalently bound to a defective, uncleaved
R; Weil, D, id 'Albesto, M. F. Ramirez, F.; de Wet, W.; Cole, W.G.; Chan, D.; Bateman, J.F.
EMBO J. 8, 1705-1710, 1989
A, Title: A base substitution in the exon of a collagen gene causes alternative splicing & A, Reference number: S09400; WUID:89356643; PMID:2767050
A;Title: Human proalpha!(I) collagen gene structure reveals evolutionary conservation of A;Reference number: A93335; MUID:84270697; PMID:6462220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: translation not shown; translated from GB/EMBL/DDBJ
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A;Status: translation not shown; translated from GB/EMBL/DDBJ
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A;Status: translatio
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Cross-references: UNIPARC:UPI000016A6FA; GB:L47667; NID:g1009093; PIDN:AAB59576.1; PID:
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                                                                                                                                 A AACCESSION 153342

A NACCESSION 15347-1357-026A

A NEGLIURE CAPPE 18870

A NACCESSION 15347-1357-026A

A NACCESSION 15347-03A

A NACCESSION 15347-13A

A N
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A;Accession: A35336
A;Molecule type: mRNA
A;Residues: 710-720, 'E', 722-737,'E', 739-745 <WAL>
A;Residues: 710-720, 'E', 722-737,'E', 739-745 <WAL>
A;Residues: 710-720, 'E', 722-737,'E', 738-745 <WAL>
A;Cross-references: UNIPARC:UPI000017384B
A;Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
A;Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
A;Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
A;Title: Severe (type III) osteogenesis imperfects due to glycine substitutions in the c
A;Accession: 154365
A;Accession: 154365
A;Accession: 154365
A;Accession: 154365
A;Accession: 154365
A;Accession: 154365
A;Residues: 746-766,'S',768-781 <FOR>
A;Residues: 746-766,'S',768-781 <FOR>
   for glycine 85 of the alpha 1(I) procollagen chain
                                           ooperative melting of intact type I collagen.
A;Reference number: I55342; MUID:92042092; PMID:1718984
           substitution of arginine
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A;Cross-references: UNIPARC:UPI000016A6FA; GB:L47667; NID:g1009093; PIDN:AAB59576.1; PID: B;Chessler, S.D.; Wallis, G.A.; Byers, P.H.
B;Chessler, S.D.; Wallis, G.A.; Byers, P.H.
G; Biol. Chem. 268, 18218-1825, 1993
A;Title: Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I) chain of tyr A;Reference number: A47426
A;Accession: A47426
A;Accession: A47426
A;Accession: A47426
A;Accession: A47426
A;Accession: B47426
A;Accession: B
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Rajandream, M.A.; Ragers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Hamlin, N.; Holroyd, S.;

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.;

Nature 393, 537-544, 1998

A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A.Attile: Deciphering the biology of Mycobacterium tuberculosis from the complete genome in A.Atcession: D70807

A.Stetus: preliminary; nucleic acid sequence not shown; translation not shown

A.Atcession: DNA

A.Residues: 1-1489 <COL>
A.Steperimental source: Strain H37Rv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B.J.; Andreassen, P.; Charbonneau,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         825 AKGEPGDAGAKGDAGPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          885 PPGPSGNAGPPGPPGPAG-----KEGGKGPRGE-----TGPAGRPGEV-----
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A; Residuces: 1179-1464 CH4>
A; Residuces: 1179-1464 CH4>
A; Cross-references: UNIPARC: UPI000017384C
A; Accession: C4426
A; Molecule type: mRNA
A; Residuces: 1179-1276, 'H', '1278-1464 CH5>
A; Accession: D47426
A; Accession: D47426
A; Accession: D47426
A; Residuces: 1179-1336, 1339-1464 CH6>
A; Residuces: 1179-1336, 1339-1464 CH6>
A; Residuces: 1179-1336, 1339-1464 CH6>
A; Residuces: UNIPARC: UPI000017384E
A; Experimental source: fetal cell 86-146
A; Accession: E47426
A; Accession: E47426
A; Residuces: 1179-1387, 'R', 1389-1464 CH7>
A; Residuces: 1179-1387, 'R', 1389-1464 CH7>
A; Cross-references: UNIPARC: UPI000017384F
A; Residuces: 1179-1387, 'R', 1389-1464 CH7>
A; Cross-references: UNIPARC: UPI000017384F
A; Residuces: 1179-1387, 'R', 1389-1464 CH7>
A; Cross-references: UNIPARC: UPI00017384F
A; Experimental source: fetal cell 88-251
A; Cross-references: UNIPARC: UPI00017384F
A; Experimental source: fetal cell 88-251
A; Experimental source: fetal cell 88-251
B; Cohn, D. H.; Apone, S.; Eyre, D. R.; Starman, B.J.; Andrease
J. Biol. Chem. 263, 14605-14607, 1988
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Pred. No. 0.00051;
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C,Superfamily: collagen alpha 1(IV) chain
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Local Similarity 37.2%;
nes 48; Conservative
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Best Local S:
Matches 48
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A Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DD. A; Residues: 1-615 <COL>
A; Residues: 1-615 <COL>
A; Cross-references: UNIPARC: UPI00000D3B10; GB:Z95207; GB:AL123456; NID:G3261745; PIDN:CAF
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A;Molecule type: DNA
A;Rosidues: 1-1212; -LIES-
A;Cross-treferences: UNIPROT: 077202; UNIPARC: UPI000007ESD0; EMBL: AF085185; NID: 93599477; I
A;Experimental source: strain Neff
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical glycine-rich protein Rv2853 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 31-Mar-2003
C;Accession: H70589
R;Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Deviin, K.; Feltwell, T.; Genter, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome and the number: A70500; MUID:98295987; PMID:9634230
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                                                                                                                                                                               64 PHGGAASGL---NG-----CCRC----GARGPESRLLEFYLAMPF---ATPMEAELAR 106
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                                                                                                                        96 GLGTPGGPGNPGGPGGLGTPGGP-GTPGGPGNPGGLGGPGNPGGPGTPGGPGTPGGOPHG
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      33; Gaps
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C;Superfamily: uncharacterized glycine-rich protein, PB motif containing
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      Indels
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                                                                                                                                                                                                                                                                                                 107 RSLAQDAPPLPV----PGVLLKEFTVSGNILTIRLT 138
                                                                                                                                                                                                                                                                                                                                                            208 -SIVTVTPPSPSVTPGGRPGSTPPATFPPGSVSTVRYT 244
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Pred. No. 0.00033;
Pred. No. 2.00033;
      65;
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9; Mismatches
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ilarity 49.3%;
Conservative
      51; Conservative
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A; Accession: T32734
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nes 35; Conserv
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Matches
      Matches
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A;Residues: 1-1901 <COL>
A;Cross-references: UNIPROT:O53553; UNIPARC:UP1000013C2A6; GB:AL022022; GB:AL123456; NID
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv3508
C;Superfamily: collagen alpha 1(IV) chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ficole, S.T.; Broech, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Comnor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom A; Reference number: A70500; MUID: 98295987; PMID: 9634230
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical glycine-rich protein Rv3508 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accesion: T32812
R;Gattung, S.; Maggi, L.
submitted to the EMBL Data Library, December 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GATGGRGPRGA
                                                                                            20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.7%; Score 151; DB 2; Length 1901; 41.1%; Pred. No. 0.00071; cive 2; Mismatches 31; Indels 20
                                 Length 1489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 2
A;Introns: 42/3; 58/1; 173/3; 268/2; 308/2; 340/1; 364/2; 387/3
                                                                                         31; Indels
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Pred. No. 0.00024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 GRGTGGSTGDADGPGGP-----GIPDGPGGNAGGPGEA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain Bristol N2; clone H17B01
                                                                                                                                                5 GRGTGGSTGDADGPGGP----GIPDGPGGNAGGPGEA
                           Score 151; DB 2;
Pred. No. 0.00057;
2; Mismatches 31;
                                                                                                                                                                                                                                                                                                                          200 Grecaccecimececacevecacerec 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 GTGGAGGPGGLIWGGGAAGGVGGAGGGTGG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74
                                                                                                                                                                                                                                                                   49 GAARASGPG----GGAPRGPHGGAASGLNG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAARASGPG----GGAPRGPHGGAASGLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: UNIPROT:061209;
                        15.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.7%;
32.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ilarity 41.1%;
Conservative
                                                                                      37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Accession: F70806
R;Cole, S.T.; Brosch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49
                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                         Matches
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15.5%; Score 148.5; DB 1; Length 1042; 29.3%; Pred. No. 0.00063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 RGSGGGGGGGGG---GGARG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 RGPHGGAASGLNGCCRCGARG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A90458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: T27525
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-297 <WILL>
A;Cross-references: UNIPROT:Q23263; UNIPARC:UPI0000077A2E; EMBL:Z49131; PIDN:CAA88979.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q19218; UNIPARC:UP1000007C4A1; EMBL:270682; PIDN:CAA94581.1;
A;Experimental source: clone F08G5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                   995 GRGAGRALPMGGGDEAPLPPVPTGPSGGPGPAGPGRGMPAGPGRGAPGPGRGGPGGPPGP 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 GQPGQDGPAGQPGAPG-PAGPEGDAGAPGAPGAPGAPGAPGAPGQRGTGLPGAPGAPGPQ 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRPGQPGSAGHPGAPGQPGSKGNNGAPGAAGGPGQPGRPGKDGQRGKGSAGAPGKAG 229
                                                                                                          45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 GTGGSTGDADGPGGPGIPDGPGGN----AGGPGBAGATGGRGPRGAGARASG-PGGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F08G5.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20605
R;Steward, C.
Submitted to the EMBL Data Library, April 1996
A;Reference number: 219299
                                                                                                                                                                                                                                                                                                                                            hypothetical protein 2C373.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27525
R;Kershaw, J.
submitted to the EMBL Data Library, April 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGGSTGDADGPGGPGIPDGPGGNAGGPGBAGATGGRGPRGAGAARASG----PGGGAPR
                                                                                                          ---TGDADGPG----GPGIPDGPGGNAGGPGEAGATGGRGP
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
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                  Score 149.5; DB 2; Length 1215;
Pred. No. 0.00061;
3; Mismatches 33; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 149; DB 2; Length 297;
Pred. No. 0.00019;
2; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37; Indels
                                                                                                                                                                                                                       1055 AGPGRG-APGPGRGAPGPSRGGPGGPPPGGRGMPPPGGRG 1093
                                                                                                                                                                                              46 RGAGAARASGPGGGAP---RGPHGGAASGLNGCCRCGARG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 149; DB 2;
Pred. No. 0.00019;
6; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: T20605
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PRGPHGGAASGLNGCCRCGARGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAGPAGG - - PGNNG - - SAGTPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: clone ZC373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.5%;
illarity 40.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 45.8%;
Matches 38; Conservative
                      15.6%;
41.0%;
Ouery Match
Best Local Similarity 41...
Best Local 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Reference number: Z20382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-299 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: CESP:ZC373.7
A;Map position: X
A;Introns: 118/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: CESP: F08G5.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 4 A; Introns: 47/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36;
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Best Local S
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Glycine-rich protein 1.0 precursor - kidney bean Glycine-rich protein 1.0 precursor - kidney bean Glycine-rich protein 1.0 precursor - kidney bean Glycine-s. Phaseolus vulgaris (kidney bean)
Glycate: 30-5ep-1998 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
Glycaesion: S01821
R.Keller, B.; Sauer, N.; Lamb, C.J.
EMBO J. 7, 3625-3633, 1988
A.Title: Glycine-rich cell wall proteins in bean: gene structure and association of the I A.Reference number: S01820, MulD:89091109; PMID:3208742
A.Reference number: S01821
A.Rocession: S01821
A.Rocession: S01821
A.Rocession: S01821
A.Residues: 1-252 <KEL>
A.Residues: 1-252 <KEL>
A.Coss-references: UNIPROT:P10495; UNIPARC:UP1000012BAFE; EMBL:X13595; NID:g21000; PIDN: G.Superfamily: Phaseolue glycine-rich protein 1.0
G.Superfamily: Phaseolue glycine-rich protein
F.1-30/Domain: signal sequence #status predicted <MAT>
F.1-30/Domain: signal sequence #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collagen alpha 1(I) chain - chicken (tentative sequence) (fragments)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 12-Aug-1981 #sequence_revision 06-Jul-1982 #text_change 31-Mar-2000
C;Accession: A90458; A90181; A02857
R;Highberger, J.H.; Corbett, C.; Dixit, S.N.; Yu, W.; Seyer, J.M.; Kang, A.H.; Gross, J. Biochemistry 21, 2048-2055, 1982
A;Fitle: Amino acid sequence of chick skin collagen alpha1(I)-CB8 and the complete prima)
A;Reference number: A90458; MUID:82231995; PMID:7093229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Experimental source: skin A, Note: this is the latest in a series of papers from these workers elucidating the sequence this is the latest in a series of papers from these workers elucidating the sequence R, Eyre, D.R., Glimcher, M.J. Blochen. Blochen. Blochen. Bloches. Res. Commun. 48, 720-726, 1972 A, Title: Evidence for a previously undetected sequence at the carboxyterminus of the alp! A, Reference number: A90181; MUID: 72243016; PMID: 5047697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A/Accession: A90181
A/Molecule type: protein
A/Rocession: A90181
A/Molecule type: protein
A/Rocession: Molecule type: protein
A/Cross-references: UNIPARC:UP10000173863
A/Experimental source: Skin
A/Cross-references: UNIPARC:UP10000173863
A/Experimental source: Skin
A/Octe: residues 1037-1042 above correspond to the carboxyl end of the protein
A/Note: residues 1037-1042 above correspond to the tripeptide repeating unit (CCComment: Most of the prolines at the third position of the tripeptide repeating unit (CCCOmment: Pro-1002 is the only 3-hydroxyproline and the only hydroxylated proline in pocysuperfamily: collagen alpha 1(1) chain: fibrillar collagen carboxyl-terminal homology;
C/Keywords: coiled coil; extracellular matrix; glycoprotein; pyroglutamic acid; trimer;
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 EGRGTGGSTGDADGPGGPGIPDGPGGNAGGPGEAGATGG--RGPRGAGAARASGPGGGAP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 15.5%; Score 148.5; DB 1;
Best Local Similarity 44.4%; Pred. No. 0.00017;
Matches 36; Conservative 3; Mismatches 37;
                                                                                                  219 GPSGNPGQDGAAGAPGQAGPAGPAGPDGQ 247
63 GPHG----GAASGINGCCRCGARGPESR 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 1-1036 <HIG>
A;Cross-references: UNIPARC:UP10000173B62
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7;	47	930	70	988	126	1034		
Gaps	RGPRG-	PAGPQGP	GGAAS-	GSAGAA	VLLKEF	GPPGP-PGPPSGGF 1034		
75;	AGATGG	AGARGE	APRGPH	-PRGPP	PLPVPG	PGP-PG		
50; Indels 75; Gaps	DGPGGNAGGPGEAGATGGRGPRG-	GPAGPPGP	AGAARASGPGGGAPRGPHGGAAS- 70	GASGPAG-	RSLAQDAP	GP		
20;	DGPG	GETGPA	AGAA	GEQGPS	EAELAR			
5; Mismatches		GPVGPAGKNGDR		GLQGPPGPPGAP	EFYLAMPFATPM	- EVGPVGPPGPP-		
5;	TIP	SAPGAP	1	SHRGFS	PESRLL	 PRGRTG		
54; Conservative	6 RGTGGSTGDADGPGGPGIP	**		931 RGDKGETGEQGDRGMKGHRGFSGLQGPPGPPGAPGEQGPSGASGPAGPRGPPGSAGAA 988	71GLNGC-CRCGARGPESRLIEFYLAMPFATPMEAELARRSLAQDAPPLPVFGVLLKEF 126	989 GKDGLNGLPGPPGPRGRIGEVGPVGPPGPP	127 TVSG 130	1035 pLDG 1038
54;	9	871 K	48	931 R	- 11	989 G	127 T	035 D
Matches	ò	ДQ	ò	QQ	ò	qq	δ	Db 1

Search completed: February 4, 2006, 12:18:10 Job time : 42 secs

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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                       Copyright
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OM protein - protein search, using sw model

February Run on:

4, 2006, 12:10:02; Search time 248 Seconds (without alignments) 512:077 Million cell updates/sec

US-09-529-206E-4

Perfect score: Title:

1 MQAEGRGTGGSTGDADGPGG......WITQCFLPVFLAQPPSGQRR 180 **BLOSUM62** Sequence:

Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 Total number of hits satisfying chosen parameters:

2166443 seqs, 705528306 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

1: uniprot_sprot:* 2: uniprot_trembl:* UniProt 05.80:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	рошо	homo	homo	homo	homo	homo	strep				mytilus		arabidor		-				Q9nhw4 nephila cla			nephila	076271 mytilus edu	093486 oncorhynchu	Q910b9 oncorhynchu	Q58my1 cyanophage	Q16988 araneus dia	Q9nhw1 nephila ina			P03211 epstein-bar
ID	CTG1B_HUMAN	Q7LBY4_HUMAN	CTAG2_HUMAN		ITBA2 HUMAN	Q5HY39 HUMAN	HYDL STRCO	Q6J6NO 9ARAC	Q5B4Q0 EMENI	Q9BIU8_ARGTR	044367 MYTED	Q8MW53 MYTGA	Q6RF45 ARATH	Q9BIU9_ARGTR	Q8I7U1_9ARAC	Q636W4_BACCZ	Q6HF99 BACHK	Q7U022_MYCBO	Q9NHW4_NEPCL	Q9L252_STRCO	044358_NEPCL	Q9NHW2_9ARAC	076271_MYTED		Q910B9_ONCMY	Q58MY1_9CAUD	Q16988 ARADI	Q9NHW1 9ARAC	IF2 STRAW	061351 DROME	EBN1_EBV
DB	-	~	-	~	Н	N	-	N	N	N	N	~	7	~	~	7	~	N	7	~	N	N	N	~	7	~	N	~	٦	~	H
% Query Match Length	180	180	210	142	143	143	627	563	617	1002	922	922	420	651	524	813	1168	1408	2249	604	871	1884	904	678	1458	597	410	626	1046	145	641
* Query Match	100.0	100.0	62.0	9.09	23.1	23.1	18.2	18.0	17.6	•	17.5	17.3	16.9	16.9	16.8	16.7	16.7	16.7	16.7	16.7	16.7	16.6	٠	16.5	16.5	16.4	16.4	16.4	16.3	16.2	16.2
Score	959	959	595	581	222	222	174.5	172.5	169	168.5	167.5	165.5	162	162	161	160.5	160.5	160.5	160.5	160	S	159.5	159	158.5	158.5	157.5	157	157	156.5	155.5	155.5
Result No.		7	m	4	ស	9	7	80	6	16	13	12	13	14.	15	16	17	18		20			23	24	25	56	27	28	29	30	31

Q777el human herpe Q8mw54 mytilus gal O1611 mytilus gal Q81wx2 bacillus an Q8mw55 mytilus gal Q8bit7 nephila ina Q6mw7 mycobacteri Q6n215 brachydanio Q6pei9 brachydanio Q6pei9 brachydanio Q6pi9 ciona intes P02453 bos taurus Q7twc0 mycobacteri Q94984 mus musculu
Q777E1 9GAWA Q8MW54_MYTGA Q81WX2_BACAN Q61W27_BACAN Q6HW27_BACAN Q9BMW5_MYTGA Q9BMW7_MYTGA Q6MW17_MYCTU Q6MW17_MYCTU Q6MX15_BRARE Q6PE19_BRARE Q6PE19_BRARE Q6PE19_BRARE Q6PE19_BRARE Q6PE19_BRARE Q6PE19_BRARE Q6PE19_BRARE Q6PE19_BRARE Q6PE19_BRARE Q6PE19_BRARE Q6PE19_BRARE Q6PE19_BRARE
00000000000000000000000000000000000000
641 9024 9024 478 481 905 1073 11073 1449 1734 1938
100 100 100 100 100 100 100 100 100 100
155.5 155.5 154.5 154.5 154.5 153 153 153.5 152.5 152.5 152.5
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                     TISSUE=Melanoma;
MEDLINE=98289662; PubMed=9626360;
Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A., de Plaen E., Boon T., an ew gene with tumor specificity.";
ILAGE-1, a new gene with tumor specificity.";
Int. J. Cancer 76:903-908(1998).
                                                                                                                                                                                                                MEDLINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914; Chen Y.-T., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S., Williamson B., Stockert E., Pfreundschuh M., Old L.J.; Hatteicular antigen aberrantly expressed in human cancers detected by autologous antibody screening."; Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                        Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-
                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
 180 AA
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EMBL; AJ003149; CAA05908.1; -; mRNA.
EMBL; AF038567; AAD05202.1; -; mRNA.
MCC; HGNC:2491; CTAGIB.
PRT;
                                                                                                     Name=CTAG1B; Synonyms=CTAG, CTAG1;
 STANDARD;
                                                                                                                    (Human)
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                                                                                                                                                                                          [1] THIS SEQUENCE.
                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                    Homo sapiens
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 CTG1B HUMAN
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NUCLEOTIDE SEQUENCE.
                    Lethe B.G.;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
"DNA methylation is the primary silencing mechanism for a set
line- and tumor-epecific genes with a CpG-rich promoter.";
Mol. Cell. Biol. 19:7327-7335(1999).
                                                                                               Length 180;
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to the EMBL/GenBank/DDBJ databases
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                                                          17992 MW; B122C5C2C8BE1569 CRC64;
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10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein)
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                                                                                             ; Score 959; DB 1;
; Pred. No. 2.2e-61;
0; Mismatches 0;
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                    Potential,
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82
    Transmembrane
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Submitted (JUL-2001)
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Submitted (MAR-2003)
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MEDLINE=21303268;
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  Antigen;
TRANSMEM
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Millahy S.J.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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"Interleukin-2-induced, melanoma-specific T cells recognize CAMEL,
unexpected translation product of LAGE-1.";
Int. J. Cancer 82:442-448(1999).
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"LAGE-1, a new gene with tumor specificity.";
Int. J. Cancer 76:903-908(1998).
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF277315; AAL27014.1; -; Genomic DNA.
EMBL; AF277315; CAB76943.1; -; Genomic DNA.
EMBL; AF277315; AAL27013.1; -; Genomic DNA.
EMBL; AF277013.1; -; Genomic DNA.
SEQUENCE 180 AA; 17992 MW; B122CSCZCBBE1569 CRC64;
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                                                                                                                                                                                                                                        100.0%; Score 959; DB 2; 100.0%; Pred. No. 2.2e-61;
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MEDLINE=98289662; PubMed=9626360;
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         Blakesley R. W., Touchman J. W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

EVENTEANATIVE PRODUCTS:
EVENTEALLETTATIVE SPIICING'S Named isoforms=2;
Name=LAGE-1B; Synonyms=LAGE-1L;
Isold=075638-1; Sequence=VSP 004301;
Isold=075638-2; Sequence=VSP 004301;
C.I. TISSUE SPECIFICITY: Testis and in some uterus samples. Observed in 25-50% of tumor samples of melanomas, non-small-cell lung carcinomas, bladder, prostate and
                                                                                                                                                                                                                                                                                                            This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in in ow way modified and this statement is not
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SEQRPGTPGPPPPEGAQGDGCRGVAFNVMFSAPHI -> IR
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 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.
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8BE0EE00AE55E8BE CRC64;
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EMBL; AJ223093; CAA11116.1; -; Genomic_DNA.
EMBL; AJ223040; CAA11043.1; -; mRNA.
EMBL; AJ223041; CAA11044.1; -; mRNA.
EMBL; AJ223041; CAA10194.1; -; mRNA.
EMBL; AJ012834; CAA10194.1; -; mRNA.
EMBL; AJ012835; CAA10196.1; -; mRNA.
EMBL; ENGO0893; AAH02833.1; -; mRNA.
ENSEMBL; ENSCO0000126890; Homo sapiens.
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121 AVLKDFTVSGNLL 133
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                                                                                                                                                                                                                                                      neck cancers.
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H-InvDB; HIX0017163; -.
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RESULT 4 Q9NY13_HUMAN

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MEDINE-22388257; PubMed=12447932; DOI=10.1073/pnas.242603899;

XX MEDINE-22388257; PubMed=124477932; DOI=10.1073/pnas.242603899;

XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wabin G.M., Hong L.,

An Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

An Ana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S.W., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S.W., Worley K.C., Hale S., Garcia A.M., Gabk R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Schwutz J., Myers R.M.,

Butkeeley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield W.S., Wonger R.W.,

Butterfield W.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield W.B., Wonger R.W.,

Butterfield W.B., Wonger R.W.,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                       Lethe B.G.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ275978; CAB76945.1; -; mRNA.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 142 AA; 13895 MW; 27EBE922AC4ACC7B CRC64;
                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.6%; Score 581; DB 2;
94.8%; Pred. No. 2.5e-34;
iive 2; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTBA2_HUMAN STANDARD; PRT; 143 AA. 014657; 081278; 181. 35, Created) 25-OCT-2004 (Rel. 45, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation update) 110-MAY-2005 (Rel. 47, Last annotation update) Name=ITBA2; Synonyms=ESO3;
                                     Hypothetical protein LAGE-2 (Fragment). Wame=LAGE-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
   Created)
(TrEMBLrel. 15, (TrEMBLrel. 15,
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                                                                                                                                                  Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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67; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 DADGPGGPGIPDGPGGNAGGPGEAGATGGRGPRGAGAARASGPGGGAP----RGPHGGAA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                           [3]
IDENTIFICATION, AND TISSUE SPECIFICITY.

FUDMed=12384295; DOI=10.1016/S0378-1119(02)00879-X;

Alpen B., Guere A.O., Scanlan M.J., Old L.J., Chen Y.-T.;

A. new member of the NY-ESO-1 gene family is ubiquitously expressed in somatic tissues and evolutionarily conserved.";
                               MEDLINE=96374823; PubMed=8786131; DOI=10.1006/geno.1996.0293; Faranda S., Frattini A., Zucchi I., Patrosso C., Milanesi L., Montagna C., Vezzoni P.; "Characterization and fine localization of two new genes in Xq28 using the genomic sequence/EST database screening approach."; Genomics 34:323-327(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DADADAG------GGADGGDGR----GGHSCRG-GVDTAAAPAGGAPPAHAPGPGRDAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26;
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                                                                                                                                                                                                                                                Gene 297:141-149(2002).
-!- TISSUE SPECIFICITY: Ubiquitous.
-!- SIMILARITY: Belongs to the CTAG family.
-!- CAUTION: Ref.2 sequence differs from that shown due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52; Indels
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
EMBL: B8396345; CAI43195.1; -; Genomic DNA.
SEQUENCE 143 AA, 14804 WW, AD164559371449F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 AA; 14804 MW; AD164559371449F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 GRILVVRWKAEDCRLLRISVINFLDQLSLVVRTWQRFGP 139
 NUCLEOTIDE SEQUENCE OF 2-143, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 GNILTIRLTAADHROLOLSISSCLOOLSLLMWITQCFLP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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Pred. No. 1.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.1%; Score 222; DB 1; 42.1%; Pred. No. 1.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC015744; AAH15744.2; -; mRNA.
EMBL; BC0662330; AAH62330.1; -; mRNA.
EMBL; X92896; CAA65489.1; ALT_FRAME; mRNA.
Ensembl; BNSG00000196976; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAY-2005 (TrEMBLrel. 30, Last sequence 10-MAY-2005 (TrEMBLrel. 30, Last annotati Lantigen family, member 3. Last Mame-LAGE3; ORFNames=XX-FW81657B9.4-001; Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSHY39_HUMAN PRELIMINARY;
QSHY39;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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Blanco G., Pereda A., Brian P., Mendez C., Chater K.F., Salas J.A.;
Blanco G., Pereda A., Brian P., Mendez C., Chater K.F., Salas J.A.;
"A hydroxylase-like gene product contributes to synthesis of a
polyketide spore pigment in Streptomyces halstedii.";
J. Bacteriol. 175:8043-8048(1993).
-!- FUNCTION: Involved in developmentally regulated synthesis of a
compound blosynthetically related to polyketide antibiotics which
is essential for spore color in Streptococcus coelicolor.
-!- COPACTOR: FAD (By similarity).
-!- SIMILARITY: Belongs to the pheA/tfdB FAD monooxygenase family.
                                                                                                                                                                                                                                           70 SGLNGCCRCGARGPESRLLEFYLAMPFATPMEAELARRSLAQDAPPLPVPGVLLKEFTVS
                                                                                                                                                       3 DADADAG------GGADGGDGR----GGHSCRG-GVDTAAAPAGGAPPAHAPGPGRDAA
                                                                           14 DADGPGGPGIPDGPGGNAGGPGEAGATGGRGPRGAARASGPGGGAP----RGPHGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21996410; PubMed=12000953; DOI=10.1038/417141a;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYDL STRCO STANDARD; PRT; 627 AA. P42534; QSS2L7;
D4.207-1995 (Rel. 32, Created)
16.007-2001 (Rel. 40, Last sequence update)
10.MAY-2005 (Rel. 47, Last annotation update)
Putative polyketide hydroxylase (EC 1.14.13.-) (WhiE ORF VIII).
OrderedLocusNames=SCO5321; ORFNames=SCGG9.12c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       130 GNILTIRLTAADHRQLQLSISSCLQQLSLLMWITQCFLP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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EMBL; X74213; CAA52289.1; -; Genomic_DNA.
PIR; T35608; T35608.
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR008160; Collagen.
Interpro; IPR002938; moase_FAD_bd.
Interpro; IPR003042; Rng hydrolase.
Interpro; IPR012336; Thioredoxin-like.
Pfam; PF01494; FAD_binding_3; 1.
PRINTS; PR00420; RNGMNOXGNASE.
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Nature 417:141-147(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .---- 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 GRGTGGSTGDADGPGGPGIPDGPGGNAGGPGEAGATGG-RGPRGAGAARASGPGGGAPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             409 GRGTGG-PGGPGGLGGPGGPGG-TGGPGGPGGPGGPDGPRGAGGAPGGGPGG----G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ren H.-L., Liu Z.-S., Pan P.-G., Wang X.-H., Ren L.-S., Bu X.-J.; bu X.-J.; bu X.-J.; bu X.-L., Liu Z.-S., Day to the EMBL/GenBank/DDBJ databases.

EMBL, AYS87193; A7387347.1; -; mRNA.

GO, GO.0005579; C:extracellular matrix (sensu Metazoa); IEA.

GO, GO.0005201; F:extracellular matrix structural constituent; IEA.

InterPro; IPR003979; tropocalastin.

PRINTS; PR01500; TR0DPOELASTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Araneoidea; Araneidae; Araneus.
                                                                                                                                                                                                                                                                                                                                                                                                  31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 PHGGAASGINGCCRCGARGPESRLLEFYLAMPF-----ATPMEAE 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------GPORGILNVALGYRYPRGAVVGADPATPVVPE 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
NCBI_TaxID=227321;
                                                                                                                                                                                                                                                                                                                      DB 1; Length 627;
                             FAD (Potential).
FAD (Potential).
R -> A (in Ref. 2).
L -> LH (in Ref. 2).
C -> S (in Ref. 2).
W; 746E84A2A9E9511C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 GRGTGGSTGDADGPGGPGIPDGPGGNAGGPGBAGATGGRGPRGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 GLGGAGAYGPGGAGPGGAĞPHGPGGPGGAĞ---PGGEĞP 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 ----ARASGPGGGAP--RGPHGGAASGLNGCCRCGARGP 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                              18.2%; Score 174.5; DB 1
42.7%; Pred. No. 0.00016;
tive 4; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       617 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  563 AA
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Flagelliform silk protein-1 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                 51 FA
319 FA
60 R
145 L
234 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSB4Q0;
10-MAY-2005 (TrEMBLrel. 30, Cr
10-MAY-2005 (TrEMBLrel. 30, Le
10-MAY-2005 (TrEMBLrel. 30, Le
Hypotherical protein.
ORFNames=AN4480.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGJGNO 9ARAC PRELIMINARY;
QGJGNO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSB4Q0_EMENI PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                        Local Similarity 42.7
es 47; Conservative
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NUCLEOTIDE SEQUENCE.
                                 22
309
60
145
234
627 AA;
proteome;
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                                 NP_BIND
CONFLICT
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                  Query Match
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06J6N0 94,
1D 06J6
AC 06J6
DT 05-J
DT
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Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,

Birran B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,

Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,

RA Butkar J., Calvo S., Farlow B., Corum B., DeArellano K.,

Biaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,

Biaz J.S., Dodge S., Graham L., Grand Pierre N., Hafez N.,

Rafer D., Johnson R., Jones C., Kanal M., Kamat A., Karatas A.,

Rells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,

Ralls C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,

Matthews C., Maucell E., McGarthy M., Meldrim J., Meneus L.,

RA Milova T., Mlenga V., Murphy T., Naylor J., Nauven C., Nicol R.,

RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,

RA Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,

Ranth C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,

Ranthas J., Tesfaye S., Theodore J., Topham K., Travers M.,

Rander B., Voung G., Zainoun J., Zembek L., Zimmer A., Zody M.,

Rander B.,

Rander B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21179804; PubMed=11283372; DOI=10.1126/science.1057561; Gatesy J., Hayashi C., Motriuk D., Woods J., Lewis R.; Extreme diversity, conservation, and convergence of spider silk fibroin sequences."
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Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Araneae,
Araneomorphae, Entelegynae, Araneoidea, Araneidae, Argiope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome Sequence of Aspergillus nidulans.";
Submitted (JAN-2004) to the BmBL/Genbank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255 GOPGHPGGPGGPGGPGGPGGPGGPGGGGGGGGGTCLCQCPCDG 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
Gatesy J.E., Hayashi C.Y.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AFISO265; AAX30594.1; -; mRNA.
GO; GO:0006737; C:cytoplasm; IEA.
GO; GO:0006817; P:phosphate transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rpothetical protein.
SQUENCE 617 AA; 58885 MW; EF073F587FEE88D2 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Flagelliform silk protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preliminary data.
EMBL; AACD01000078; EAA60823.1; -; Genomic_DNA.
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Lucas J.M., Vaccaro E., Waite J.H.; "A molecular, morphometric and mechanical comparison of the structural elements of byssus from Mytilus edulis and Mytilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 GRGTGGSTGDADGPGGPGIPDGPGGNA--GGPGEAGATGGRGPRGAGAARASGPGGGAPR
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Xiao Y., Smith S.R., Ishmael N., Ayele M., Kumar N., Redman J.,
Riedmuller S., Uterback T., Whitelaw C.A., Fraser C.M., Town C.D.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Underwood B.A., Xiao Y., Moskal W., Torian U., Redman J., Wu H.C., Utterback T., Town C.D.;
"Arabidopsis thaliana ORF clones of hypothetical genes.";
"Arabidopsis thaliana ORF clones of hypothetical genes.";
Submitted (UUN-2014) to HeBL/GenBank/DDBJ databases.
EMBL; AX501356; AAR99368.1; -; mRNA.
InterPro: IPR020383; MATH.
Pfam; PF00917; AAT6924.1; -; mRNA.
InterPro: IPR020183; MATH.
SMORGI; MATH; 2.
PROSITE; PS70144; MATH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilinae; Mytilus.
NCBL_TaxID=29158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 17.3%; Score 165.5; DB 2; Length 922; Best Local Similarity 47.6%; Pred. No. 0.00099; Matches 39; Conservative 1; Mismatches 29; Indels 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 420;
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expireNCE 420 AA; 44404 MW; 6B108942B389EEA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA281AE0975BB7D4 CRC64;
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Last annotation update)
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50.0%; Pred. No. 0.00086;
tive 0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               420 AA
                                                                                                                                                                                                                                                                                     galloprovincialis ";
J. Exp. Biol. 205:1807-1817 (2002).

EMBL; AF44826; AAM34601.1; -; mRNA.
GO; GO:0005737; C:cytoplasm; IEA.
InterPro; IPR008160; Collagen.
Pfam, PF01391; Collagen; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
ORFNames=At2g04170;
Arabidopsis thaliana (Mouse-ear cress).
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05-JUL-2004 (TrEMBLrel. 27, Last seq
01-FEB-2005 (TrEMBLrel. 29, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 GPPGPA------GPQGPB 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 GPHGGAASGLNGCCRCGARGPE 84
                                                                                                                                                                            MEDLINE=22038007; PubMed=12042339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      922 AA; 80750 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGRF45_ARATH PRELIMINARY;
QGRF45;
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Best Local Similarity 50.0
Matches 42; Conservative
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                                                                                                                                               NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                           48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28
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                                                                                                                                                                                                                                                                                                     5 GRGTGGSTGDADGPGGPGIPDGPGGNAG-----GPGEAG-----ATGGRGPRGA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Foot;
MEDLINE=98070444; PubMed=9405478; DOI=10.1074/jbc.272.51.32623;
Qin X.X., Coyne K.J., Waite J.H.;
"Tough tendons. Mussel byssus has collagen with silk-like domains.";
J. Biol. Chem. 272:32623-32627 [1997).
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=preCol-D;
Mytlius edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilinae; Mytilus.
                                                                                                                                                                                                                                             19;
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                                                                                                                                                                            17.6%; Score 168.5; DB 2; Length 1002; 44.3%; Pred. No. 0.00065; tive 1; Mismatches 34; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               th 17.5%; Score 167.5; DB 2; Length 922; Similarity 41.4%; Pred. No. 0.00071; 41; Conservative 5; Mismatches 32; Indels 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qin X., Coyne K.J., Waite J.H.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF020293, AAB96638.1; -; mRNA.
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0006817; P:phosphate transport; IEA.
InterPro; IFR008160; Collagen.
Pfam; PF01391; Collagen.
                                                                                                                  1002 AA; 75889 MW; 432D73E1EDF6A88A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 922 AA; 80306 MW; 599D155E47A2C24A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Precollagen D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 FGPGGAGGFGPGGAGGFGPGGAGGYGPGGAGG 237
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Mytilus galloprovincialis (Mediterranean mussel).
                                                                                                                                                                                                                                                                                                                                                                                                                                    49 ---GAARASGPGGGAPRGPHGGAASGLNGCCRCGARG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----GAPRGPHG-GAASGINGCC-----RCGARGPE
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                InterPro; IPR008160; Collagen.
NON TER 1 1
NON TER 1002
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Q8MW53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 044367 MYTED PRELIMINARY;
044367;
                                                                                                                                                                                                                                          43; Conservative
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                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21179804; PubMed=11283372; DOI=10.1126/science.1057561; Gatesy J., Hayashi C., Motriuk D., Woods J., Lewis R.; Extreme diversity, conservation, and convergence of spider silk fibroin sequences."; Science 291:2603-2605(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Argiope trifasciata (Banded garden spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Araneoidea; Araneidae; Argiope.
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Araneomorphae; Entelegynae; Araneoidea; Araneidae; Araneus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 16.9%; Score 162; DB 2; Length 651; Best Local Similarity 44.0%; Pred. No. 0.0013; Matches 37; Conservative 2; Mismatches 37; Indels
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UJUN-2003 (TrEMBLrel. 24, Last annotation update)
Major ampullate gland dragline silk protein-1 (Fragment).
Araneus ventricosus.
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NUCLEOTIDE SEQUENCE.
Gatesy J.E., Hayashi C.Y.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF350264; AAK30593.1; -; mRNA.
NON_TER 1
NON_TER 77CEEC8757DE48DA CRC64;
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Liu Z.-S., Ren H.-L., Pan F.-G.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, X174110; AAN85280.1; -; mENA.
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0006817; P:phosphate transport; IEA.
InterPro; IPR008160; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                       651 AA
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                                         60 APRGPHGGAASGLNGCCRCGARGP 83
                                                                                                                        75 - PRGPRPGGGGGPGPWSGPRGP 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last seq 01-WAR-2003 (TrEMBLrel. 23, Last ann Flagelliform silk protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                       PRT;
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Q9BIU9;
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Flag;
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0981109 ARC
10081101 ARC
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249 GPGAGGAPGGFGGPGGPGGPGGPGG-PGGPGGAAGGAGGVGPGGGSSGGAGGAGPVSV 307
                                                                                                                                                                              5 GRGTGGSTGDADGPGGPGIPDGPGGNAGGPGEA------GATGGRGPRG---- 47
                                                                                                                          28; Indels 32; Gaps
                                                                                                                                                                                                                                                                                                                308 SSSVVVSGAGGPSGPGAGGVGPGRAGPGGIYGPGAGGLYGPGAGGSFGP 357
                                                                                                                                                                                                                                                                                   48 -----AGAARASGPGGG-----APRGPHG-GAASGINGCCRCGARGP 83
                                                                      Length 524;
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42492 MW; 7437FB39892422F2 CRC64;
                                                                    16.8%; Score 161; DB 2;
40.0%; Pred. No. 0.0012;
tive 6; Mismatches 28
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Matches 44; Conservative
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completed: February 4, 2006, 12:17:23

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                                                                                                                                                                                                                                                                                               February 4, 2006, 12:17:37 ; Search time 50 Seconds (without alignments) 297.632 Million cell updates/sec
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(c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                 Copyright
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100.0%; Pred. No. 9.7e-79;
tive 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DATABLE FORM:
COMPUTER: DATABLE FORM:
SOUTHWER IN PATENT Release #1.0, Version #1.25
SUGNERNY APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: VAN AMSLECTAM, JOHN R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7005
TELECHMONICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Leth, Bernard
APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITER OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
US-08-963-825-18

US-09-50-811-18

US-09-548-608-18

US-10-153-469A-10

US-10-153-469A-10

US-10-158-887-9

US-09-285-887-9

US-09-2131-347-2-21

US-09-010-928B-4

US-09-010-928B-4

US-09-010-928B-4

US-08-642-255-80

US-08-642-255-80
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PCT-US96-06229-16
                                                                                                                                                                                                                                                                                                                                                   US-09-297-269-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Wolf, Greenfield & Sacks, P.C. STREET: 600 Atlantic Avenue CITY: Boston STATE: MA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08791495
Patent No. 5811519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 180 amino acids
TYPE: amino acid
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Best Local Similarity 100.
Matches 180; Conservative
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61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAELARRSLAGDAPPLPVPG 120
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/165,546D
FILING DATE: 02-0ct-1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1996
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 10,946
REFERENCE/DOCKET NUMBER: 10,946
REFERENCE/DOCKET NUMBER: 10,946
TELECOMMUNICATION NUMBER: 10,946
TELECOMMUNICATION SEQ ID NO. 6723432 aman D.
TELECOMMUNICATION SEQ ID NO. 6723400
TELEFAX: (212) 318-3400
TELEFAX: (212) 318-3400
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100.0%; Score 959; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 9.7e-79;
Matches 180; Conservative 0; Mismatches 0; Indels
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Sequence 9, Application US/09341829A

Patent No. 6794131

GENERAL INFORMATION:

APPLICANT: Letth, Bernard

APPLICANT: Locas, Sophie

APPLICANT: Boon-Falleur, Thierry

APPLICANT: Godelaine, Daniele

APPLICANT: Godelaine, Daniele

APPLICANT: Godelaine, Daniele

APPLICANT: Homer APPLICATION UNMBER: US/09/341,829A

CURRENT APPLICATION NUMBER: US/09/341,829A

CURRENT FILING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: PCT/US98/01445

PRIOR APPLICATION NUMBER: PCT/US98/01445

SOFTWARE: FastSEQ for Windows Version 3.0

LENNORM: LENNORM: LOCAL LOC
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100.0%; Pred. No. 9.7e-79;
tive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 180; Conservative
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ORGANISM: Homo sapiens
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US-09-341-829A-9
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Patent No. 6723832

GENERAL INFORMATION:
APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAELARRSLAQDAPPLPVPG 120
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                                     61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAELARRSLAQDAPPLPVPG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25, Application US/09392714A

Sequence 25, Application US/09392714A

Patent No. 668147

GENERAL INFORMATION:

APPLICANT: Geanlan, Matthew J.

APPLICANT: Ganlan, Matthew J.

APPLICANT: Chen, Yao-Teeng

APPLICANT: Chen, Yao-Teeng

APPLICANT: Old, Lloyd J.

TITLE OF INVENTION: Therefor

FILE REFERENCE: L0461/7062

CURRENT APPLICATION NUMBER: US/09/392,714A

CURRENT FILING DATE: 1999-09-09

EARLIER PELING DATE: 1998-07-15

NUMBER OF SEQ ID NOS: 30

SOUTH NOS: 30

SOUTH NOS: 20

SOUTH NOS: 20
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MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 959; DB 2; Best Local Similarity 100.0%; Pred. No. 9.7e-79; Matches 180; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-09-392-714-25
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US-09-165-546D-15
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LENGTH: 180
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CITY: New York City STATE: New York
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                                                      PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAELARRSLAQDAPPLPVPG 120
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1 MQAEGRGTGGSTGDADGPGGPGGPGIPDGPGGNGGPGEAGATGGRGPRGAGARASGPGGGA 60
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APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
TITLE OF INVENTION: ITSELF, AND USES THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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100.0%; Pred. No. 9.7e-79;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Scanlan, Matthew J.
APPLICANT: Scanlan, Matthew J.
APPLICANT: Old, Lloyd J.
APPLICANT: Stockert, Bilsabeth
APPLICANT: Chen, Yao-Tseng
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REFERENCE: L0461/7105 (JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 30
SECTUMARE: PatentIn version 3.0
SEQ ID NO 30
LENGTH: 180
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                                                                                                                                                                                                                                                                                              ; Sequence 30, Application US/09849602; Patent No. 6794501; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08937263B
Patent No. 6274145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 666 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 180; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York City STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-30
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US-09-849-602-30
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US-08-937-263B-8
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61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAELARRSLAQDAPPLPVPG 120
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APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Stockert, Routh, Ago-teeng; Scanlan, Matthew;
APPLICANT: Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Associated Proteins, Uses Thereof,
TITLE OF INVENTION: Binding Peptides Derived Therefrom
TITLE OF INVENTION: Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.4%; Score 953; DB 2;
99.4%; Pred. No. 3.4e-78;
iive 0; Mismatches 1;
SCFURARE: WordPerfect
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/937,263B
FILING DATE: September 15, 1997
FRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/72,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sin, Eric, Patent Agent
REGISTRATION NUMBER: 40,177
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 1D NO: 8:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 09/062,422
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; Sequence 8, Application US/09751798
; Patent No. 6525177
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PRIOR APPLICATION DATA:
PEPLICATION NUMBER: 08/725,11
FILING DATE: OCTOBER 3, 1996
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SOPTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OS
FILING DATE:
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Matches 179; Conservative
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Pred. No. 3.4e-78;
0; Mismatches 1; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
FILING DATE:
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APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Godelaine, Daniele
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CARRESPONDENCE ADDRESS:
CARRESPONDENCE 
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600 Atlantic Avenue
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6525,77man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEPHONE: (212) 318-3168
TELEPHONE: (212) 752-5958
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: Van Ameteerdam, John R.
REGISTRATION NUMBER: 40,212
REPERENCE/DOCKET NUMBER: L0461/7005
TELECOMMUNICATION:
TELEPHONE: 617-720-3500
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Patent No. 5811519
GENERAL INPORMATION:
APPLICANT: Leth, Bernard
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity 99.4'
Matches 179; Conservative
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                                                                                                                                                                                                                                                                                                                                              ...rr: amino acid
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TOPOLOGY: linear
US-09-751-798-8
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; Sequence 7, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
    APPLICANT: Leth., Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT PILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; TENNER OF SEQ ID NOS: 14
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  DB 1; Length 180;
                                             15; Indels
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Patent No. 5811519
GENERAL INFORMATION:
APPLICANT: Lett, Bernard
APPLICANT: Locas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEGUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
84.9%; Score 814; DB 1, 84.4%; Pred. No. 1e-65;
Query Match 84.9%; Score 814; DB 'Best Local Similarity 84.4%; Pred. No. 1e-65 Matches 152; Conservative 13; Mismatches
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-341-829A-7
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US-08-791-495-5
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MOAEGRGTGGSTGDADGPGGPG1 PDGPGGNAGGPGEAGATGGRGPRGAGAARASGPGGGA
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121 AVLKDFTVSGNLLFMSVRDQD 141
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REGISTRATION NUMBER: 28977
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INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
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52.4%;
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Best Local Similarity 52.43
Matches 43; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                               US-09-010-928B-28
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US-09-010-928B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Beon-Falleur, Thierry
TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
FILE REFERENCE: L0461/706
CURRENT APPLICATION NUMBER: US/09/341,829A
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US/08/791,495
PRIOR APPLICATION NUMBER: PCT/US98/01445
NUMBER OF SEQ ID NOS: 14
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Indels
                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.4%; Score 589; DB 1 76.6%; Pred. No. 2e-45;
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76.6%; Pred. No. 2e-45;
iive 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Mismatches
                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY FAGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461
TELECOMUNICATION INFORMATION:
TELEPANCE: 617-720-350
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 210 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 76.69
Matches 108; Conservative
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Best Local Similarity 76.6
Matches 108; Conservative
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MOLECULE TYPE: protein
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                                                                            02210
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LENGTH: 210
TYPE: PRT
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                                     STATE: N
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61 PRGPHGGAASAQDGRCPCGGARRPDSRLLQLHITMPPSSPMEAELVRRILSRDAAPLPRPG 120
                                                                                                              61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAELARRSLAQDAPPLPVPG 120
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                                                    1 MOAEGOGTGGSTGDADGPGGPGTPDGPGGNAGGPGEAGATGGRGPRGAARASGPRGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 28, Application US/09010928B
Patent No. 5994099
GENERAL INFORMATION
APPLICANT: Lewis, Randolph V
APPLICANT: Hayashi, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWRY, KOLASCH & BIRCH
STREET: 8110 GATEHOUSE RD. SUITE 500E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V
APPLICANT: Hayashi, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 745;
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STATE: VIRGINIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Pred. No. 2.9e-06;
1; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,928B
FILING DATE: 22-JAN-1998
CLASSIFICATION: 435
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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/642,255
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Best Local Similarity 41.7%; Pred. No. 8.8e-06;
Matches 43; Conservative 5; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CIASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND. Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A5556-3/BIR
TELECOMMUNICATION INFORMATION:
TELEBARNE: (415) 494-8771
TELERAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 72:
                                                                                                                                                                                                                                                                                                                                                                                                                          3 AEG-RGTGGSTGD----ADGPGGPG
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                    TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 633 amino acids
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 41.7%;
Matches 43; Conservative
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linear
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                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-642-255-73
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STRANDEDNESS: single
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STRANDEDNESS: si
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94111-4187
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; Sequence 73, Application US/08642255
; Patent No. 5773249
; GENERAL INFORMATION:
    APPLICANT: CAPPELLO, Joseph
    APPLICANT: PERRARI, Franco A.
    TITLE OF INVENTION: High Molecular Weight Collagen-Like
    TITLE OF INVENTION: Protein Polymers
    TITLE OF INVENTION: Protein Polymers
    TITLE OF INVENTION: 135
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: FLERR, HOHBACH, TEST, ALBRITTON & HERBERT
    STREET: 4 Embarcadero Center, Suite 3400
    CITY: San Francisco
    CITY: San Francisco
    CONTANTION: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.7%; Score 160; DB 1; Length 870; ilarity 52.4%; Pred. No. 3.4e-06; Conservative 1; Mismatches 32; Indels
                                                                                                                         CITY: FALLS
STATE: VIRGINIA
COMPUTRY: UNITED STATES OF AMERICA
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CUMRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,928B
FILING DATE: 22-JAN-1998
CLASSIFICATION:
NAME: Murphy Jr., Gerald M
REFERENCE/DOCKET NUMBER: 1847-109P
REFERENCE/DOCKET NUMBER: 28977
REFERENCE/DOCKET NUMBER: 1447-109P
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
'TWATH: 870 amino acids
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APPLICATION NUMBER: US/08/642,255
                                                                     SEE: BIRCH, STEWART, KOLASCH & BIRCH: 8110 GATEHOUSE RD. SUITE 500E FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, BETLYAM I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: 455556-3/BIR
CODING THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     691 GPGGAGGSYGLGGAGGSGGVGP 712
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ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-09-010-928B-2
                    NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
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Best Local Similarity
Matches 43; Conserv
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                                                                     ADDRESSEE:
STREET: 81
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Score 156.5; DB 1; Length 633;
Pred. No. 4.9e-06;
5; Mismatches 24; Indels 31; Gaps
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Sequence 72, Application US/08642255

Patent No. 5773249

Patent No. 5773249

PAPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, Franco A.

TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                           ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                             45 PRG----AGAARASGPGGGAPRGPHGGAASGLNGCCRCGARGP 83
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3 AEG-RCTGGSTGD-----ADGPGGPG------IPDGPGGNAGGPGEACATGGRG 44
8 6 8 6
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-	215 AQGPAGPGGSRGDPGPPGAQGPAGPGGSRGDPGPPGAQGPAGPGGSRGDPGPPGAHGPAG 274		
-	PAGPGGSRGDPC		
	SSRGDPGPPGAOC	•	
-	GAOGPAGPG		
	GSRGDPGPP		
	AQGPAGPG		
	215		•

Search completed: February 4, 2006, 12:19:06 Job time : 51 secs

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RESULT
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Sequence 71, Appl
Sequence 74, Appl
Sequence 386, App
Sequence 139, App
Sequence 11, Appl
Sequence 15, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 11, Appl
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7, Appli
3, Appli
3, Appli
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8, Appli
                                                4, 2006, 12:29:28; Search time 174 Seconds (without alignments) 432.237 Million cell updates/sec
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                                                                                             1 MQAEGRGTGGSTGDADGPGG......WITQCFLPVFLAQPPSGQRR 180
                                                                                                                                                                                                                                                                                                                               Description
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/cgn2_6/ptcdata/1/pubpaa/US08_PUBCOMB.pep:*
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/cgn2_6/ptcdata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptcdata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptcdata/1/pubpaa/US10A_PUBCOMB.pep:*
       GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                  Published Applications AA Main:*
                                                                                                                                1867569 seqs, 417829326 residues
                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                    protein search, using sw model
                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                               seq length: 0
seq length: 200000000
                                                                               US-09-529-206E-4
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Match Length
              Copyright
                                                  February
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Maximum DB &
                                    OM protein
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                                  69, Appl
834, App
834, App
17, Appli
388, Appl
141, App
88, Appl
76, Appl
76, Appl
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77, Appl
17, Appl
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APPLICANT: Hayden-Ledbetter, Martha S.

AITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 4266
                                                                    Sequence
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Pred. No. 1.8e-67;
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APPLICANT: Old, Lloyd J.
APPLICANT: Stockert, Elisabeth
APPLICANT: Chen, Yao-Teach
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REFERENCE: L0461/7105 (JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 30
SEQ ID NOS: 30
LENGTH: 180
LENGTH: 180
LENGTH: 180
TYPE: PAT
ORCANISM: Homo sapiens
US-09-849-602-30
US-11-067-064-75
US-11-067-159-75
US-10-166-473-639
US-10-296-734-834
US-10-87-373-7
US-10-295-027-388
US-10-188-832-141
US-10-188-832-141
US-10-177-937-76
US-10-177-937-76
US-11-067-064-76
US-10-777-053-17
US-10-777-053-17
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100.0%; Pre
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Publication No. US20030165834A1
GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
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Publication No. US20030118592A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 180; Conserv
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; Publication No. US20030215425A1
; GERREAL INFORMATION:
APPLICANT: Simard, John J. L.
APPLICANT: Diamond, David C.
TITLE OF INVENTION: PRESENTING CELLS
TITLE OF INVENTION: PRESENTING CELLS
TITLE OF INVENTION: PRESENTING CELLS
CURRENT APPLICATION NUMBER: US/10/026,066
CURRENT APPLICATION NUMBER: 09/561,074
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR PLILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
SOFTWARE: Patentin version 3.0
SEQ ID NO 71
LENGTH: 180
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ORGANISM: Homo sapiens
US-10-026-066-3
                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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RESULT 4 US-10-117-937-74

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61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAELARRSLAQDAPPLPVPG 120
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APPLICANT: Afar, Daniel
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Warson, Susan R.
APPLICANT: Warson, Susan R.
APPLICANT: Wasson, Susan R.
APPLICANT: Worker of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Exceening for Modulators of Cancer, TITLE OF INVENTION: Methods of Screening for Modulators of Cancer, CURRENT APPLICATION NUMBER: US 09/663,733
FRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR PILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/334,393
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               Sequence 386, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
Application US/10117937
No. US20030220239A1
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ORGANISM: Homo sapiens
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Matches 180; Conservative
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CORGANISM: Homo sapiens
US-10-188-832-139
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US-10-777-053-11
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PRIOR APPLICATION NUMBER: US 60/340,376

PRIOR FILING DATE: 2001-12-14

PRIOR PELING DATE: 2002-01-108

PRIOR PELING DATE: 2002-01-108

PRIOR APPLICATION NUMBER: US 60/347,349

PRIOR APPLICATION NUMBER: US 60/355,250

PRIOR APPLICATION NUMBER: US 60/355,250

PRIOR PILING DATE: 2002-02-08

PRIOR PILING DATE: 2002-02-08

PRIOR PILING DATE: 2002-02-13

PRIOR PILING DATE: 2002-02-13

PRIOR SPING APPLICATION NUMBER: US 60/356,714

PRIOR SPING APPLICATION NUMBER: US 60/356,714

PRIOR SPING APPLICATION NUMBER: US 60/356,714

PRIOR PILING DATE: 2002-02-13

NUMBER OF SEQ ID NOS: 1386

SOFTWARE: PATENTIN Ver. 2.1
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Publication No. US20040054137A1

GENERAL INFORMATION:
APPLICANT: Thompson, Scott A

APPLICANT: Ramshaw, Ian A

TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REFERENCE: Savine
CURRENT APPLICATION NUMBER: US/10/296,734

CURRENT PILING DATE: 2003-08-04

PRIOR PILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 1507

SOFTHARE: Patentin Version 3.2

LENGTH: 180
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100.0%; Score 959; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 180; Conservative
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US-10-295-027-386
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US-10-296-734-832
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Sequence 11, Application US/10777053

Publication No. US20040132088A1

GENERAL INFORMATION:

APPLICANT: Simard, John J. L.

APPLICANT: Diamond, David C.

TITLE OF INVENTION: TRAGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN

TITLE OF INVENTION: TRAGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN

TITLE OF INVENTION: TRAGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN

FILE REFERENCE: MANNK, 022C1

CURRENT FILING DATE: 2004-02-10

PRIOR APPLICATION NUMBER: 60/336,968

PRIOR PLING DATE: 2002-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 979

SOFTWARE: FREUSEQ for Windows Version 4.0
                                                                                                                                                                    Sequence 139, Application US/10188832

Sequence 139, Application US/10188832

Sequence 139, Application No. US20040076955A1

GENERAL INFORMATION:
APPLICANT: Mack, David H.

APPLICANT: Aziz, Natasha
APPLICANT: Bos Biotechnology, Inc.
TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
FILE OF INVENTION: Cancer
CURRENT APPLICATION NUMBER: US 60/302,814
PRIOR FILING DATE: 2001-07-03
PRIOR PELLING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: US 60/310,099
PRIOR PELLING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-13
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121 VILKEFTVSGNILTIRLTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQPPSGQRR 180
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Sequence 11, Application US/10837217
Sequence 11, Application US/10837217
Publication No. US20040203051A1
GENERAL INFORMATION:
APPLICANT: Simard, John J. L.
APPLICANT: Diamond, David C.
APPLICANT: Diamond, David C.
APPLICANT: Diamond, David C.
APPLICANT: Diamond, David C.
APPLICANT: Diamond, SAPRESSION VECTORS ENCODING EPITOPES OF TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN FILE REPERENCE: MANNK. 0.2.2.2
CURRENT APPLICATION NUMBER: US/10/837,217
CURRENT FILING DATE: 2004-04-30
PRIOR FILING DATE: 2002-11-07
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100.0%; Score 959; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0;
Score 959; DB 4;
Pred. No. 1.8e-67;
; Mismatches 0;
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Publication No. US20040180354A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Simmard, John J. L.
APPLICANT: Diamond, David C.
APPLICANT: Liu, Liping
APPLICANT: Liu, Liping
APPLICANT: Liu, EPHTOPE SEQUENCES
FILE REFERENCE: MANNK. 032A
CURRENT APPLICATION NUMBER: 05/409123
PRIOR APPLICATION NUMBER: 60/409123
PRIOR FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 610
SOFTWARE: FRASEQ for Windows Version 4.0
SEQ ID NO 74
100.0%; Scc
100.0%; Pre
tive 0; }
    Query Match 100.
Best Local Similarity 100.
Matches 180; Conservative
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ORGANISM: Homo sapiens
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US-10-657-022-74
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Publication No. US20040158044A1
GENERAL INFORMATION: LOSON ALExader; Jager, Elke; Chen, Yao, Scanlan, Matt;
APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
USES THEREOF
USES THEREOF
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REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 318-3400
                                                                                                                                                                       Indels
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MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
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0
                                                                                                                     100.0%; Score 959; DB 4;
100.0%; Pred. No. 1.8e-67;
iive 0; Mismatches 0;
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APPLICATION NUMBER: US/09/165,546D
FILING DATE: 02-0ct-1998
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: FULBRIGHT & JAWORSKI LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/751,088
FILING DATE: 02-Jan-2004
CLASSIFICATION: 530
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SEQUENCE DESCRIPTION: SEQ ID NO: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
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OPERATING SYSTEM: PC-DOS
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TYPE: amino acid
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CORRESPONDENCE ADDRESS:
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                                                                                                                        Query Match
Best Local Similarity 100.
Matches 180; Conservative
                             TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10158
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US-10-751-088-15
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Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma Modulators
FILE REPERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR PILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1270
LENGTH: 180
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Sequence To Application US/10871708

Publication No. US20050118186A1

GENERAL INFORMATION:

APPLICANT: Chiang, Chih-Sheal

TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED

TITLE OF INVENTION: ANTIGENS IN COMPOSITIONS FOR VARIOUS TYPES OF CANCERS FILE REFERENCE: MANNK. 035A

CURRENT APPLICATION NUMBER: US/10/871,708

CURRENT FILING DATE: 2004-06-17

PRIOR APPLICATION NUMBER: 60/479,554

PRIOR FILING DATE: 2003-06-17

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 959; DB 5;
100.0%; Pred. No. 1.8e-67;
ive 0; Mismatches 0;
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ORGANISM: Autoimmunogenic Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 180; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CORGANISM: Homo sapiens
US-10-723-860-1270
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Best Local Similarity
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                                                                                                                                                                                                                                                                                 Length 180;
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Sequence 9, Application US/1087373
Fublication No. US20040234541A1
GENERAL INFORMATION:
APPLICANT: Leth, Bernard
APPLICANT: Lotas, Sophie
APPLICANT: De Smet, Charless
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
TITLE OF INVENTION: LO461/7066
CURRENT APPLICATION NUMBER: US/10/877,373
CURRENT APPLICATION NUMBER: US/09/341,829
PRIOR APPLICATION NUMBER: US/09/341,829
PRIOR APPLICATION NUMBER: US/09/341,829
PRIOR APPLICATION NUMBER: PCT/US98/01445
NUMBER OF SEQ ID NOS: 14
NUMBER OF SEQ ID NOS: 14
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Pred. No. 1.8e-67;
0; Mismatches 0;
     PRIOR APPLICATION NUMBER: 60/336,968
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 979
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%;
Matches 180; Conservative 0
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                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo Sapien
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Best Local Similarity
Matches 180; Conserv
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LENGTH: 180
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RESULT 13 US-10-723-860-1270 ; Sequence 1270, Application US/10723860

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61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAELARRSLAQDAPPLPVPG 120
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100.0%; Score 959; DB 5; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels
US-10-895-523-3

US-10-895-523-3

US-10-895-523-3

Publication No. US20050130920A1

GENERAL INFORMATION:

APPLICANT: Simard, John J. L.

APPLICANT: Diamond, David C.

TITLE OF INVENTION: PRESENTING CELLS

TITLE OF INVENTION: PRESENTING CELLS

FILE REFERENCE: MANNK.021CP1CC1

CURRENT FILING DATE: 2004-07-20

PRIOR APPLICATION NUMBER: 10/026,066

PRIOR APPLICATION NUMBER: 10/05,905

PRIOR PILING DATE: 2001-12-07

PRIOR FILING DATE: 2001-12-07

PRIOR FILING DATE: 2000-04-28

PRIOR FILING DATE: 2001-04-27

PRIOR PILING DATE: 2001-04-27

PRIOR FILING DATE: 2001-04-28

PRIOR PRIOR PRIOR DATE: 2001-04-28

PRIOR PRIOR PRIOR DATE: 2001-04-28

PRIOR PRIOR DATE: 2001-04-28

PRIOR PRIOR DATE: 2001-04-28
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TYPE: PRT

ORGANISM: Homo sapiens
US-10-895-523-3
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Sequence 7, Appli
Sequence 28, Appl
Sequence 1, Appli
Sequence 145, App
Sequence 243, Appl
Sequence 28, Appl
Sequence 28, Appli
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135, App
152, App
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Sequence 33, Appl
Sequence 163, App
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131.828 Million cell updates/sec
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/cgn2_6/ptodata/2/pubpaa/US08 NEW PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US1_NEW PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US1_NEW PUB.pep:*
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US-11-01-00-6821-234-1096

US-11-052-554A-135

US-11-052-554A-135

US-11-052-554A-136

US-10-995-561-911

US-10-995-561-912

US-10-995-561-913

US-10-995-561-913

US-10-995-561-913

US-11-052-554A-149

US-11-052-554A-161

US-11-052-554A-161

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Maximum Match 100%
Listing first 45 summaries
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Sequence 146, App		Sequence 964, App	Sequence 148, App	Sequence 1431, Ap	4.1	Sequence 160, App	Sequence 34, Appl	Sequence 26, Appl		Sequence 329, App	Sequence 7, Appli	Sequence 32, Appl	Sequence 167, App	Sequence 164, App	Sequence 147, App	Sequence 165, App	Sequence 35, Appl		Sequence 150, App
US-11-052-554A-146	US-11-052-554A-166	US-10-821-234-964	US-11-052-554A-148	US-10-821-234-1431	US-11-186-284-31	US-11-052-554A-160	US-11-029-003-34	US-11-186-284-26	US-11-052-554A-154	US-11-124-368A-329	US-10-841-129-7	US-11-060-659-32	US-11-052-554A-167	US-11-052-554A-164	US-11-052-554A-147	US-11-052-554A-165	US-11-186-284-35	US-11-052-554A-144	US-11-052-554A-150
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138	137.5	137.5	135.5	135.5	135.5	134.5	134	133.5	133	131.5	131	131	130.5	130.5	130.5	129	129	128.5	128
26	2.1	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 7, Application Us/11155288

Publication No. US20060008468A1

GENERAL INFORMATION:
APPLICANT: Chiang, Chih-sheng
APPLICANT: Simard, John J.L.
ITILE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
ITILE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS;
FILE REFERENCE: MANNK.050A
CURRENT APPLICATION NUMBER: 08/11/155,288
CURRENT FILING DATE: 2005-06-17
PRIOR FILING DATE: 2004-06-17
PRIOR FILING DATE: 2004-06-17
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FRAESEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 2.3e-78;
Matches 180; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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JS-11-155-288-7
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Sequence 28, Application US/11021441
Publication No. US20050249748A1
GENERAL INFORMATION:
APPLICANT: DUBENSKY, Thomas W., Jr.
APPLICANT: LUCKETT, William S., Jr.
APPLICANT: COOK, David N.

US-11-021-441-28

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Sequence 243, Application US/11000463 Publication No. US20050266423A1 GENERAL INFORMATION:
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                                               63 GPHGGAASGLNGCCRCGARG 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Chen, Rui-hong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-052-554A-145
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INVENTION: RECOMBINANT NUCLBIC ACID MOLECULES,
INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 RGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAELARRSLAQDAPPLPVPGV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 QAEGRGTGGSTGDADGPGGPGIPDGPGGNAGGPGEAGATGGRGPRGAGAARASGPGGGAP 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 AEGRGTGGSTGDADGPGGPGIPDGPGGNAGGPGEAGATGGRGPRGAGAARASGPGGGAPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/10848976

Publication No. US20050260564A1

GENERAL INPORMATION:

APPLICANT: Sugden, Bill

APPLICANT: Wang, Jindong

APPLICANT: Wang, Jindong

APPLICANT: WARF - Wisconsin Alumni Research Foundation

TITLE OF INVENTION: A Non-Cytotoxic oriP Replicon

FILE REFRENCE: 800.041US1

CURRENT FILING DATE: 2004-05-19

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO:

LENGTH: 641
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Pred. No. 1e-06;
1; Mismatches
TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID ITILE OF INVENTION: EXPRESSION CASSETTES, ANITILE OF INVENTION: THEREOF CURRENT APPLICATION NUMBER: US/11/021,441 CURRENT APPLICATION NUMBER: US/11/021,441 CURRENT FILING DATE: 2004-12-23 CORP. PRIOR PILING DATE: 2004-10-06 CORP. PRIOR PILING DATE: 2004-10-06 CORP. PRIOR PILING DATE: 2004-10-01 CORP. PRIOR PILING DATE: 2004-00-06 CORP. PRIOR PILING DATE: 2004-00-05 CORP. PRIOR PILING DATE: 2004-00-05 CORP. PRIOR PILING DATE: 2004-07-23 CORP. PRIOR PILING DATE: 2004-07-23 CORP. PRIOR PILING DATE: 2004-07-30 CORP. PRIOR PILING DATE: 2004-03-26 CORP. PRIOR P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Fusion protein US-11-021-441-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.2%;
ilarity 46.2%;
Conservative
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; ORGANISM: Epstein-Barr virus
US-10-848-976-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
hes 37; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 28
LENGTH: 240
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Best Local S:
Matches 37
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NS-11-052-554A-145

Sequence 145, Application US/11052554A

Publication No. US20050288866A1

Sequence 145, Application US/11052554A

Hublication No. US20050288866A1

Sequence 145, Application No. US2005028886A1

THIRE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN-LIKE

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN-LIKE

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

PILE REFERENCE: 30853/40359A

CURRENT FILING DATE: 2005-02-07

PRIOR FILING DATE: 2004-07-20

PRIOR PILING DATE: 2004-07-20

PRIOR PILING DATE: 2004-07-06

NUMBER OF SEQ ID NOS: 763

SOFTWARE: Patentin version 3.3

SEQ ID NO 145

LENGTH: 1079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22
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APPLICANT: Wang, Zhiwei
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Cao, Yi-Cheng
APPLICANT: Drmanac, Radole T.
APPLICANT: Drmanac, Radole T.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 785CIP4CN
CURRENT APPLICATION NUMBER: 10/291,265
PRIOR FILING DATE: 2002-11-09
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/921,209
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/911,404
PRIOR FILING DATE: 2000-01-25
PRIOR PLILNG DATE: 2000-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

16.0%; Score 153; DB 7;
Best Local Similarity 43.3%; Pred. No. 2.9e-06;
Matches 39; Conservative 2; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            540 NGGAAGKGGAGGQGGTGGGTGGQGGAGGDG 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mycobacterium tuberculosis H37Rv
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Sequence 1096, Application US/10821234

Publication No. UG20050255114A1

Sequence 1096, Application US/10821234

Publication No. UG20050255114A1

GENERAL INFORMATION:

APPLICANT: Labat, Ivan

APPLICANT: Stache-Crain, Birgit

APPLICANT: Tang, Y. Tom

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

FILE REPERENCE: 812A

CURRENT APPLICATION NUMBER: US/10/821,234

CURRENT FILING DATE: 2004-04-07

PRIOR PELING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 P----GGGAPRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAELARRSLAQ 111
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        ---TGPAGRPGEV---
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Pred. No. 5.5e-06;
4; Mismatches 42;
                                                                                                                                                                                                                                Sequence 2, Application US/11021603
; Sequence 2, Application US/11021603
; Bublication No. US20060003954A1
; GENERAL INFORMATION:
    APPLICANT: Beri, Rajinder
    TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES
; TITLE REFERENCE: 06275-254US1
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/11/021,603
; CURRENT FILING DATE: 2002-06-10
; PRIOR FILING DATE: 2002-06-10
; PRIOR FILING DATE: 2002-12-12
; PRIOR FILING DATE: 1999-12-15
; PRIOR FILING DATE: 1999-12-15
; NUMBER: OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 4.0
; LENGIN O A
        ---KEGGKGPRGE--
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        885 PPGPSGNAGPPGPPGPAG---
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37.2%;
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Best Local Similarity 37.2%;
Matches 48; Conservative
                                                              112 DAPPLPVPG 120
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; ORGANISM: Homo sapiens
US-10-821-234-1096
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-821-234-1096
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APPLICANT: MILLENILUM FARTMACEULICAIB, INC.
APPLICANT: Kanatkar, Shubhangi
APPLICANT: Kanatkar, Shubhangi
APPLICANT: Kanatkar, Shubhangi
APPLICANT: Kanatkar, Shubhangi
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, AND
TITLE OF INVENTION: THIRAPY OF COLON CANCER
FILE REFERENCE: MPMOI-029P2RNM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-01-21
PRIOR FILING DATE: 2002-11-21
PRIOR PELICATION NUMBER: US 60/361,978
PRIOR PELING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SECTION NUMBER: PRESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                 35;
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 37.2%; Pred. No. 5.5e-06;
Matches 48; Conservative 4; Mismatches 42; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 15.8%; Score 151.5; DB 7; Length 1464; 1 Similarity 37.2%; Pred. No. 5.5e-06; 48; Conservative 4; Mismatches 42; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Millennium Pharmaceuticals, Inc. APPLICANT: Berger, Allison APPLICANT: Guillemette, Tracy L.
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTHARE: FastSEQ for Windows Version 3.0
LENGTH: 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28, Application US/11186284 Publication No. US20050266493A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 DAPPLPVPG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             923 -GPPGP-PG 929
                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-243
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Best Local Similarity
Matches 48; Conserval
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us-09-529-206e-4.rapbn

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Sequence 138, Application US/11052554A

Sequence 138, Application US/11052554A

Publication No. US20050288866A1

GENERAL INFORMATION:
APPLICANTY Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROFIEINS OF THERAPEUTIC POTENTIAL
TITLE OF INVENTION: PROFIEINS OF THERAPEUTIC POTENTIAL
TITLE OF INVENTION: DATE: 2005-02-07

CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-02-06

PRIOR FILING DATE: 2004-02-06

NUMBER OF SEQ ID NOS: 763

SOFTWARE: Patentin version 3.3

SOFTWARE: Patentin version 3.3
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDITONAND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOCTWARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 911
LENGTH: 1767
                                                                                                                                                  523 GNGTGGVNGADNTINPDTPGGAGEPGGAGGAGGAGGPGGTGGTGGNGGNGGNGGNG 582
                                                                                                                         7 GTGGSTGDADGPGGPGIPDGPGGNAGG--PGEAGATGGRGPRGA-GAARASGPGGGAPRG
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                     Length 615;
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Pred. No. 1.9e-05;
8; Mismatches 45;
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                  15.6%; Score 149.5; DB 7;
49.3%; Pred. No. 3.3e-06;
tive 5; Mismatches 26;
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Best Local Similarity 35.4%;
Matches 45; Conservative 8
                  Query Match
Best Local Similarity 49.3<sup>3</sup>
Matches 35, Conservative
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US-11-052-554A-138
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FILE REFERENCE: 30853/40359A

CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT PILING DATE: 2005-02-07

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR APPLICATION NUMBER: IN 173/DEL/2004

PRIOR APPLICATION NUMBER: 10 173/DEL/2004

PRIOR APPLICATION NUMBER: 10 33

SOFTWARE: Patentin version 3.3

SOFTWARE: Patentin version 3.3

SEQ ID NO 152
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TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR PILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: Patentin version 3.3
SEQ ID NO 135
LENGTH: 1901
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                                                                                                    828 AKGEPGDAGAKGDAGPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVG 887
                                                                                                                                                       56 P----GGGAPRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAELARRSLAQ 111
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Gaps
35;
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42; Indels
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Pred. No. 8e-06;
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4; Mismatches
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US-11-052-554A-135
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  Conservative
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Best Local Similarity
Matches 45; Conserv
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US-10-995-561-915
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                                                                                                                             -----GKPGPEG-----LRGIPGPVGEQGLPGAAGODGPPG 1393
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Publication No. US20050272054A1
GENERAL INFORMATION:
FULL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
FILE REPERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PAPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20050272054A1
GENERAL INFORMATION:
GENETICANT: CARGILL,
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 912
                                                                                         57 GGGAPRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAELARRSLAQDAPPL 116
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                 GTGGSTGDADGPGGPGI-----PDGPGGNAGGPGEAGATGGRGPRGA-GAARASG-P 56
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Pred. No. 1.9e-05;
8; Mismatches 45;
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Best Local Similarity 35.4%;
Matches 45; Conservative
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ORGANISM: Homo sapiens
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US-10-995-561-914
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US-10-995-561-912
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
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                                            7 GTGGSTGDADGPGGPGI-----PDGPGGNAGGPGEAGATGGRGPRGA-GAARASG-P
29; Gaps
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45; Indels
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Pred. No. 1.9e-05
8; Mismatches
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35.4%;
45; Conservative
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Job time: 17 secs
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CORGANISM: Homo sapiens
US-10-995-561-915
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